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(54) Title: GLIAL CELL LINE-DERIVED NEUROTROPHIC FACTOR RECEPTOR (57) Abstract <p>The present invention relates to glial cell line-derived neurotrophic factor (GDNF), a potent neurotrophin that exhibits a broad spectrum of biological activities on a variety of cell types from both the central and peripheral nervous systems. The present invention involves the cloning and characterization of a high affinity receptor for GDNF. This molecule has been named GDNF receptor (GDNFR) since it is the first known component of a receptor system. Nucleic acid and amino acid sequences are described for GDNFR protein products. A hydrophobic domain with the features of a signal peptide is found at the amino terminus, while a second hydrophobic domain at the carboxy terminus is involved in the linkage of the receptor to the cell membrane. The lack of a transmembrane domain and cytoplasmic region indicates that GDNFR requires one or more accessory molecules in order to mediate transmembrane signaling. GDNFR mRNA is widely distributed in both nervous system and non-neural tissues, consistent with the similar distribution found for GDNF.</p>		

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GLIAL CELL LINE-DERIVED NEUROTROPHIC FACTOR RECEPTOR

1. Field of the Invention

The present invention relates to receptors for glial cell line-derived neurotrophic factor (GDNF) and provides nucleic acid and amino acid sequences encoding GDNF receptor (GDNFR). The present invention also relates to therapeutic techniques for the treatment of GDNF-responsive conditions.

2. Background of the Invention

Glial Cell line-Derived Neurotrophic Factor

Glial cell line-derived neurotrophic factor (GDNF) was initially isolated and cloned from rat B49 cells as a potent neurotrophic factor that enhances survival of midbrain dopaminergic neurons (Lin et al., Science, 260, 1130-1132, 1993). Recent studies have indicated that this molecule exhibits a variety of other biological activities, having effects on several types of neurons from both the central and peripheral nervous systems. In the central nervous system (CNS), GDNF has been shown to prevent the axotomy-induced death of mammalian facial and spinal cord motor neurons (Li et al., Proceedings Of The National Academy Of Sciences, U.S.A., 92, 9771-9775, 1995; Oppenheim et al., Nature, 373, 344-346, 1995; Yan et al., Nature, 373, 341-344, 1995; Henderson et al., Science, 266, 1062-1064, 1994; Zurn et al., Neuroreport, 6, 113-118, 1994), and to rescue developing avian motor neurons from natural programmed cell death (Oppenheim et al., 1995 supra). Local administration of GDNF has been shown to protect nigral dopaminergic neurons from axotomy-induced (Kearns and Gash, Brain Research, 672, 104-111, 1995; Beck et al., Nature, 373, 339-341, 1995) or neurotoxin-induced degeneration (Sauer et al., Proceedings Of The National Academy Of Sciences U.S.A., 92, 8935-8939, 1995; Tomac et al., Nature, 373, 335-339, 1995). In addition, local administration of GDNF has been shown to induce sprouting from dopaminergic neurons, increase levels of dopamine, noradrenaline, and serotonin, and improve motor behavior (Tomac et al., 1995 supra).

More recently, GDNF has been reported to be a potential trophic factor for brain noradrenergic neurons and Purkinje cells. Grafting of fibroblasts ectopically expressing GDNF prevented 6-hydroxydopamine-induced degeneration and promoted the phenotype of adult noradrenergic neurons in vivo (Arenas et al., Neuron, 15, 1465-1473, 1995), while exogenously applied GDNF effectively promoted survival

and morphological differentiation of embryonic Purkinje cells in vitro (Mount et al., Proceedings Of The National Academy Of Sciences U.S.A., 92, 9092-9096, 1995). In the peripheral nervous system, GDNF has been shown to promote the survival of neurons in nodose, ciliary, and sympathetic ganglia, as well as small populations of embryonic sensory neurons in dorsal root ganglia (DRG) and trigeminal ganglia (Trupp et al., Journal Of Cell Biology, 130, 137-148, 1995; Ebendal et al., Journal Of Neuroscience Research, 40, 276-284, 1995; Oppenheim et al., 1995 supra; Yan et al., 1995 supra; Henderson et al., 1994 supra). GDNF has also been reported to enhance the expression of vasoactive intestinal peptide and preprotachykinin-A mRNA in cultured superior cervical ganglion (SCG) neurons, and thus effects the phenotype of SCG neurons and induces bundle-like sprouting (Trupp et al., 1995 supra).

Expression of GDNF has been observed in a number of different cell types and structures of the nervous system. In the CNS, GDNF mRNA expression has been observed by reverse transcriptase polymerase chain reaction (RT-PCR) in both developing and adult rat striatum, the major target of nigral dopaminergic innervation, and widely in other regions, including hippocampus, cortex, thalamus, septum, cerebellum, spinal cord, and medulla oblongata (Arenas et al., supra 1995; Poulsen et al., Neuron, 13, 1245-1252, 1994; Springer et al., Experimental Neurology, 127, 167-170, 1994; Stroemberg et al., Experimental Neurology, 124, 401-412, 1993; Schaar et al., Experimental Neurology, 124, 368-371, 1993). In human, GDNF transcripts have also been detected in striatum, with highest level in the caudate and lower levels in the putamen. Detectable levels are also found in hippocampus, cortex, and spinal cord, but not in cerebellum (Schaar et al., Experimental Neurology, 130, 387-393, 1994; Springer et al., 1994 supra). In the periphery, GDNF mRNA expression has been reported in DRG and SCG of postnatal day 1 rats, sciatic nerve, and primary cultures of neonatal Schwann cells (Trupp et al., 1995 supra; Hoffer et al., Neuroscience Letters, 182, 107-111, 1994; Henderson et al., 1994 supra; Springer et al., 1994 supra). In addition, recent studies have shown that GDNF transcripts are also widely expressed in peripheral non-neuronal organs, including postnatal testis and kidney, embryonic whisker pad, stomach, and skin. Expression can be detected at lower levels in embryonic muscle, adrenal gland and limb bud, and in postnatal lung, liver and ovary (Trupp et al., 1995 supra; Henderson et al., 1994 supra). So far, however, the biological significance of the non-neuronal expression of GDNF is not clear.

Detailed descriptions of the preparation and characterization of GDNF protein products may be found in U.S. Patent Application No. 08/182,183 filed May 23, 1994 and its parent applications (also see PCT/US92/07888, WO 93/06116 filed

September 17, 1992 and European Patent Application No. 92921022.7, Publication No. EP 610 254) the disclosures of which are hereby incorporated by reference. Additional GDNF protein products are described in pending U.S. Patent Application No. 08/535,681 filed September 28, 1995, the disclosure of which is hereby
5 incorporated by reference. As used herein, the term "GDNF protein product" includes biologically active synthetic or recombinant GDNF proteins and analogs, as well as chemically modified derivatives thereof. GDNF analogs include deletion variants such as truncated GDNF proteins, as well as insertion and substitution variants of GDNF. Also included are GDNF proteins that are substantially homologous to the human
10 GDNF protein.

GDNF Therapy

GDNF therapy is helpful in the treatment of nerve damage caused by conditions that compromise the survival and/or proper function of one or more types
15 of nerve cells. Such nerve damage may occur from a wide variety of different causes. Nerve damage may occur to one or more types of nerve cells by: (1) physical injury, which causes the degeneration of the axonal processes and/or nerve cell bodies near the site of injury; (2) temporary or permanent cessation of blood flow to parts of the nervous system, as in stroke; (3) intentional or accidental exposure to neurotoxins,
20 such as chemotherapeutic agents (e.g., cisplatin) for the treatment of cancer or dideoxycytidine (ddC) for the treatment of AIDS; (4) chronic metabolic diseases, such as diabetes or renal dysfunction; or (5) neurodegenerative diseases such as Parkinson's disease, Alzheimer's disease, and amyotrophic lateral sclerosis (ALS), which result from the degeneration of specific neuronal populations.

25 Several studies indicate that GDNF therapy is particularly helpful in the treatment of neurodegenerative conditions such as the degeneration of the dopaminergic neurons of the substantia nigra in Parkinson's disease. The only current treatments for Parkinson's disease are palliative, aiming at increasing dopamine levels in the striatum. The expected impact of GDNF therapy is not simply to produce an
30 increase in the dopaminergic neurotransmission at the dopaminergic nerve terminals in the striatum (which will result in a relief of the symptoms), but also to slow down, or even stop, the progression of the degenerative processes and to repair the damaged nigrostriatal pathway and restore its function. GDNF may also be used in treating other forms of damage to or improper function of dopaminergic nerve cells in human
35 patients. Such damage or malfunction may occur in schizophrenia and other forms of psychosis. The only current treatments for such conditions are symptomatic and require drugs which act upon dopamine receptors or dopamine uptake sites, consistent

with the view that the improper functioning of the dopaminergic neurons which innervate these receptor-bearing neuronal populations may be involved in the disease process.

5 Receptors

A number of receptors which mediate binding and response to protein factors have been characterized and molecularly cloned, including receptors for insulin, platelet derived growth factor, epidermal growth factor and its relatives, the fibroblast growth factors, various interleukins, hematopoietic growth factors and ciliary
10 neurotrophic factor (U.S. 5,426,177). Study results indicate that some receptors can bind to multiple (related) growth factors, while in other cases the same factor can bind and activate multiple (related) receptors (e.g., Lupu et al., Science, 249:1552-1555, 1990; Dionne et al., EMBO J., 9:2685-2692, 1990; Miki et al., Science, 251:72-75, 1991). Most receptors can broadly be characterized as having an extracellular portion
15 or domain responsible for specifically binding a protein factor, a transmembrane domain which spans the cell membrane, and an intracellular domain that is often involved in initiating signal transduction upon binding of the protein factor to the receptor's extracellular portion. Although many receptors are comprised of a single polypeptide chain, other receptors apparently require two or more separate subunits in
20 order to bind to their protein factor with high-affinity and to allow functional response following binding (e.g., Hempstead et al., Science, 243:373-375, 1989; Hibi et al., Cell, 63:1149-1157, 1990).

The extracellular and intracellular portions of a given receptor may share common structural motifs with the corresponding regions of other receptors,
25 suggesting evolutionary and functional relationships between different receptors. These relationships can often be quite distant and may simply reflect the repeated use of certain general domain structures. For example, a variety of different receptors that bind unrelated factors make use of "immunoglobulin" domains in their extracellular portions, while other receptors utilize "cytokine receptor" domains in their factor-
30 binding regions (e.g., Akira et al., The FASEB J., 4:2860-2867, 1990). A large number of receptors with distinct extracellular binding domains (which thus bind different factors) contain related intracytoplasmic domains encoding tyrosine-specific protein kinases that are activated in response to factor binding (e.g., Ullrich and Schlessinger, Cell, 61:203-212, 1990). The mechanisms by which factor-binding
35 "activates" the signal transduction process is poorly understood, even in the case of receptor tyrosine kinases. For other receptors, in which the intracellular domain encodes a domain of unknown function or in which the binding component associates

with a second protein of unknown function (e.g., Hibi et al., Cell, 63:1149-1157, 1990), activation of signal transduction is not well characterized.

The mode of action of GDNF in vivo is not clearly elucidated in the art, in part due to the absence of information on a receptor for GDNF. Two groups have
5 independently found that striatum injected [¹²⁵I]-labeled GDNF can be retrogradely transported by dopaminergic neurons in the substantia nigra (Tomac et al., Proceedings Of The National Academy Of Sciences Of The United States Of America. 92, 8274-8278, 1995; Yan et al., 1995 supra). Retrograde transport of [¹²⁵I]-GDNF by spinal cord motor neurons, DRG sensory neurons and neurons in the B layer of
10 retina ganglia was also been observed. These retrograde transport phenomena can all be specifically inhibited by 100-fold or higher concentrations of unlabeled GDNF, suggesting a saturable, receptor-mediated transport process. In vitro, recombinant GDNF has been shown to enhance the survival and promote dopamine uptake of cultured dopaminergic neurons at very low concentrations. The observed half-
15 maximal effective concentration (EC₅₀) of GDNF on these neurons is 0.2 to 1.6 pM (Lin et al., 1993 supra). GDNF has also been shown to support the survival of dissociated motor neurons at low concentrations. The reported EC₅₀ of GDNF on motor neurons, in a 5 to 10 fM range, is even lower than that on dopaminergic neurons (Henderson et al., 1994 supra).

20 Taken together, these observations indicate that receptor(s) for GDNF expressed in these cells have very high ligand binding affinities. Similar to members of the TGF- β family, the widely diversified tissue distribution and varied biological function of GDNF on different populations of cells suggest that different types of receptor(s) for GDNF or receptor complexes may exist. Saturation steady-state and
25 competitive binding of [¹²⁵I]-GDNF to E10 chick sympathetic neurons has shown that these neurons express GDNF binding sites differing from those observed in dopaminergic and motor neurons. The half maximal saturation concentration and the half-maximal inhibition concentration of GDNF on these binding sites is in the range of 1 to 5 nM (Trupp et al., 1995 supra). Similarly, the EC₅₀ of GDNF in supporting
30 the survival of sympathetic neurons from P1 rat SCG has also been reported to be in the nanomolar range (Trupp et al., 1995 supra).

To better understand the mechanism by which GDNF activates signal transduction to exert its affects on cells, it would be beneficial to identify the receptor(s) which mediate binding and response to this protein factor. It would also be
35 beneficial for GDNF therapy to identify and make possible the production of accessory molecules which provide for or enhance GDNF signal transduction. Moreover, the identification of a protein receptor for GDNF would provide powerful applications in

diagnostic uses, for example, as an aid in determining if individuals would benefit from GDNF protein therapy. Furthermore, the protein receptor for GDNF could be a key component in an assay for identifying additional molecules which bind to the receptor and result in desired biological activity.

5

SUMMARY OF THE INVENTION

The present invention provides nucleic acid sequences which encode a
10 neurotrophic factor receptor protein having an amino acid sequence as depicted in
Figures 2 and 4 (SEQ. ID. NOs.: 2 and 4) as well as biologically equivalent analogs.
The neurotrophic factor receptor protein and protein products of the present invention
are designated herein as glial cell line-derived neurotrophic factor receptor (GDNFR)
protein and protein products. The novel GDNFRs are functionally characterized by
15 the ability to bind GDNF specifically and with high affinity, and to act as part of a
molecular complex which mediates or enhances the signal transduction affects of
GDNF. GDNFR protein products are typically provided as a soluble receptor protein
and in a substantially purified form.

In one aspect, the present invention provides for the production of GDNFR
20 protein products by recombinant genetic engineering techniques. In an alternative
embodiment, the GDNFR proteins are synthesized by chemical techniques, or a
combination of the recombinant and chemical techniques.

In another aspect of the present invention, the GDNFR proteins may be made
in glycosylated or non-glycosylated forms. Derivatives of GDNFR protein typically
25 involve attaching the GDNFR protein to a water soluble polymer. For example, the
GDNFR protein may be conjugated to one or more polyethylene glycol molecules to
decrease the precipitation of the GDNFR protein product in an aqueous environment.

Yet another aspect of the present invention includes the various polynucleotides
encoding GDNFR proteins. These nucleic acid sequences are used in the expression
30 of GDNFR in a eukaryotic or prokaryotic host cell, wherein the expression product or
a derivative thereof is characterized by the ability to bind to GDNF and thereby form a
complex capable of mediating GDNF activity, such as increasing dopamine uptake by
dopaminergic cells. The polynucleotides may also be used in cell therapy or gene
therapy applications. Suitable nucleic acid sequences include those specifically
35 depicted in the Figures as well as degenerate sequences, naturally occurring allelic
variations and modified sequences based on the present invention.

Exemplary nucleic acid sequences include sequences encoding a neurotrophic

factor receptor protein comprising an amino acid sequence as depicted in Figures 2 and 4 (SEQ ID NOs. 2 and 4) capable of complexing with glial cell line-derived neurotrophic factor (GDNF) and mediating cell response to GDNF, and biologically equivalent analogs thereof. Such sequences include: (a) a sequence set forth in Figure 1 (SEQ ID NO. 1) comprising nucleotides encoding Met¹ through Ser⁴⁶⁵ or Figure 3 (SEQ ID NO. 3) comprising nucleotides encoding Met¹ through Ser⁴⁶⁸ encoding a neurotrophic factor receptor (GDNFR) capable of complexing with glial cell line-derived neurotrophic factor (GDNF) and mediating cell response to GDNF; (b) a nucleic acid sequence which (1) hybridizes to a complementary sequence of (a) and (2) encodes an amino acid sequence with GDNFR activity; and (c) a nucleic acid sequence which but for the degeneracy of the genetic code would hybridize to a complementary sequence of (a) and (2) encodes an amino acid sequence with GDNFR activity. Also disclosed herein are vectors such nucleic acid sequences wherein the sequences typically are operatively linked to one or more operational elements capable of effecting the amplification or expression of the nucleic acid sequence. Host cells containing such vectors are also contemplated. Typically, the host cell is selected from mammalian cells and bacterial cells, such as a COS-7 cell or E. coli, respectively.

A further aspect of the present invention involves vectors containing the polynucleotides encoding GDNFR proteins operatively linked to amplification and/or expression control sequences. Both prokaryotic and eukaryotic host cells may be stably transformed or transfected with such vectors to express GDNFR proteins. The present invention further includes the recombinant production of a GDNFR protein wherein such transformed or transfected host cells are grown in a suitable nutrient medium, and the GDNFR expressed by the cells is, optionally, isolated from the host cells and/or the nutrient medium. The present invention further includes the use of polynucleotides encoding GDNFR and vectors containing such polynucleotides in gene therapy or cell therapy.

The host cell may also be selected for its suitability to human implantation, wherein the implanted cell expresses and secretes a neurotrophic factor receptor of the present invention. The host cell also may be enclosed in a semipermeable membrane suitable for human implantation. The host cell may be transformed or transfected ex vivo. An exemplary device for treating nerve damage involves: (a) a semipermeable membrane suitable for implantation; and (b) cells encapsulated within the membrane, wherein the cells express and secrete a neurotrophic factor receptor as disclosed herein. The membrane is selected from a material that is permeable to the neurotrophic factor receptor protein but impermeable to materials detrimental to the encapsulated cells.

Methods for the recombinant production of a neurotrophic factor receptor of the present invention are also disclosed. An exemplary methods involves: (a) culturing a host cell containing a nucleic acid sequence encoding a neurotrophic factor receptor of the present invention, such as an amino acid sequence depicted in Figures 2 and 4 (SEQ ID NOs. 2 and 4) capable of complexing with glial cell line-derived neurotrophic factor (GDNF) and mediating cell response to GDNF, or biologically equivalent analogs thereof; (b) maintaining said host cell under conditions suitable for the expression of said neurotrophic factor receptor by said host cell; and (c) optionally, isolating said neurotrophic factor receptor expressed by said host cell. The host cell may be a prokaryotic cell or a eukaryotic cell. If bacterial expression is involved, the method may further include the step of refolding the neurotrophic factor receptor.

The present invention includes an isolated and purified protein comprising an amino acid sequence as depicted in Figures 2 and 4 (SEQ ID NOs. 2 and 4) capable of complexing with glial cell line-derived neurotrophic factor (GDNF) and mediating cell response to GDNF, and biologically equivalent analogs thereof. Exemplary analogs include, but are not limited to, proteins comprising the amino acid sequence Ser¹⁸ through Pro⁴⁴⁶, Asp²⁵ through Leu⁴⁴⁷ and Cys²⁹ through Cys⁴⁴² as depicted in Figure 2 (SEQ ID NO:2) as well as proteins comprising the amino acid sequence Met¹⁷ through Pro⁴⁴⁹ and Cys²⁹ through Cys⁴⁴³ as depicted in Figure 4 (SEQ ID NO:4). The proteins of the present invention may be glycosylated or non-glycosylated and may be produced by recombinant technology or chemical synthesis. The present invention further includes nucleic acid sequences encoding a receptor protein comprising such amino acid sequences.

Also disclosed herein are pharmaceutical compositions comprising a protein receptor of the present invention in combination with a pharmaceutically acceptable carrier. A variety of other formulation materials may be used to facilitate manufacture, storage, handling, delivery and/or efficacy.

Another aspect of the present invention includes the therapeutic use of GDNFR genes and proteins. For example, a circulating or soluble GDNFR protein product may be used alone or in conjunction with GDNF in treating disease of or injury to the nervous system by enhancing the activity of transmembrane signaling of GDNF. Thus, the proteins and pharmaceutical compositions of the present invention may be used in treating improperly functioning dopaminergic nerve cells, Parkinson's disease, Alzheimer's disease and amyotrophic lateral sclerosis. Alternatively, a recombinant GDNFR gene may be inserted in the cells of tissues which would benefit from increased sensitivity to GDNF, such as motor neurons in patients suffering from amyotrophic lateral sclerosis. In yet another embodiment, GDNFR may be used to

block GDNF activity in cases where GDNF activity is thought to be detrimental. The GDNFR may be used to verify that observed effects of GDNF are due to the GDNFR.

In another aspect of the invention, GDNFR probes may be used to identify cells and tissues which are responsive to GDNF in normal or diseased states.

- 5 Alternatively, the probes may be used to detect an aberrancy of GDNFR expression in a patient suffering from a GDNF-related disorder.

In a further aspect of the invention, GDNFR probes, including nucleic acid as well as antibody probes, may be used to identify GDNFR-related molecules. For example, the present invention provides for such molecules which form a complex with GDNFR and thereby participate in GDNFR function. As another example, the present invention provides for receptor molecules which are homologous or cross-reactive antigenically, but not identical to GDNFR.

The present invention also provides for the development of both binding and functional assays for GDNF based on the receptor. For example, assay systems for detecting GDNF activity may involve cells which express high levels of GDNFR, and which are therefore extremely sensitive to even very low concentrations of GDNF or GDNF-like molecules. In yet another embodiment, soluble GDNFR may be used to bind or detect the presence of GDNF or GDNF-like molecules.

In addition, the present invention provides for experimental model systems for studying the physiological role of GDNF. Such systems include assays involving anti-GDNFR antibodies or oligonucleotide probes as well as animal models, such as transgenic animals which express high levels of GDNFR and therefore are hypersensitive to GDNF or animals derived using embryonic stem cell technology in which the endogenous GDNFR genes were deleted from the genome. An anti-GDNFR antibody will binds a peptide portion of the neurotrophic factor receptor proteins. Antibodies include monoclonal and polyclonal antibodies. Alternatively, immunological tags for which antibodies already exist may be attached to the GDNFR protein to aid in detection. Such tags include but are not limited to Flag (IBI/Eastman Kodak) and myc sequences. Other tag sequences such as polyhistidine have also been used for detection and purification on metal chelating columns.

30 Additional aspects and advantages of the invention will be apparent to those skilled in the art upon consideration of the following description, which details the practice of the present invention.

BRIEF DESCRIPTION OF THE FIGURES

Figure 1 depicts a nucleic acid sequence (SEQ ID NO:1) encoding human glial cell line-derived neurotrophic factor receptor (GDNFR). The amino acid sequence of the full length GDNFR protein is encoded by nucleic acids 540 to 1934.

Figure 2 depicts the amino acid sequence (SEQ ID NO:2) of the full length human GDNFR protein.

Figure 3 depicts a nucleic acid sequence (SEQ ID NO:3) encoding rat GDNFR. The amino acid sequence of the full length GDNFR protein is encoded by nucleic acids 302 to 1705.

Figure 4 depicts the amino acid sequence (SEQ ID NO:4) of the full length rat GDNFR protein

Figure 5 depicts the alignment and comparison of portions of GDNFR cDNA sequences produced in various clones as well as the consensus sequence for human GDNFR.

Figure 6 depicts the identification of Neuro-2A derived cell lines expressing GDNFR.

Figure 7A and 7B depict the results of the equilibrium binding of [125 I]GDNF to cells expressing GDNFR.

Figure 8 depicts the results of the chemical cross-linking of [125 I]GDNF to GDNFR and Ret Expressed in cells expressing GDNFR.

Figure 9 depicts the results of the induction of c-Ret autophosphorylation by GDNF in cells expressing GDNFR.

Figure 10 depicts the results of the induction of c-Ret autophosphorylation by GDNF and soluble GDNFR.

Figure 11 depicts the results of the blocking of c-Ret autophosphorylation by a Ret-Fc fusion protein.

Figure 12 depicts the results of the induction of c-Ret autophosphorylation by GDNF in motor neurons.

5 Figure 13 depicts a model for GDNF signaling mediated by GDNFR and Ret.

DETAILED DESCRIPTION OF THE INVENTION

10 Glial cell line-derived neurotrophic factor (GDNF) is a potent neurotrophic factor which exhibits a broad spectrum of biological activities on a variety of cell types from both the central and peripheral nervous systems. It is a glycosylated, disulfide-linked dimer which is distantly related (less than 20% homology) to the transforming growth factor- β (TGF- β) superfamily. GDNF's ability to enhance the survival of
15 dopaminergic neurons and other neuron populations demonstrates its therapeutic potential for the treatment of Parkinson's disease as well as other forms of nerve damage or malfunction.

 In contrast to the extensive studies on the distribution and bioactivity of GDNF, there have been no reports on the identification of a receptor or receptors
20 which mediate binding of GDNF to a cell and thereby mediate intracellular signaling and a cell response. The present invention is based upon the discovery of a high affinity receptor first found on the surface of cultured retinal cells from postnatal rats. These receptors possess an estimated GDNF binding affinity comparable to that of the receptors found in dopaminergic and motor neurons; midbrain dopaminergic neurons
25 (Lin et al., 1993 supra; Sauer et al., 1995 supra; Kearns and Gash, 1995 supra; Beck et al., 1995 supra; Tomac et al., 1995a supra), facial and spinal cord motor neurons (Li et al., 1995 supra; Oppenheim et al., 1995 supra; Yan et al., 1995 supra; Zurn et al., 1994 supra; Henderson et al., 1994 supra). The receptor molecule has been
30 named GDNF receptor (GDNFR) since it is the first known component of a receptor system for GDNF. The present invention also provides the first description of the expression cloning and characterization of GDNFR protein. Cells modified to express the recombinant receptor bind GDNF with high affinity.

 Using a dopamine uptake assay and [125 I]-GDNF binding on cultured cells, high affinity receptors to GDNF were detected on the surface of rat photoreceptor
35 cells. As further described in the Examples, the study of photoreceptor cells lead to the isolation of a cDNA clone by expression cloning for GDNF receptor. The nucleic acid sequence for GDNFR encodes a protein of 468 amino acids with 31 cysteine

residues and three potential N-glycosylation sites. Next, a nucleic acid sequence from the rat cDNA clone was used to isolate its human homolog which was found to be nearly identical to the rat receptor at the amino acid level. The human GDNFR cDNA sequence encodes a protein of 465 amino acids with the positions of all cysteine
5 residues and potential N-glycosylation sites conserved relative to the rat receptor. This high degree of primary sequence conservation indicated an important role for this receptor in the biological function of GDNF.

As discussed above, many receptors have three main domains: an extracellular or cell surface domain responsible for specifically binding a protein factor; a
10 transmembrane domain which spans the cell's membrane; and an intracellular or cytoplasmic domain that is typically involved in initiating signal transduction when a protein factor binds to the extracellular domain. It was determined, however, that GDNFR is unrelated in sequence or structural characteristics to any known protein (such as the consensus sequences found in either receptor kinases or cytokine
15 receptors), lacks a cytoplasmic domain, lacks the C-terminal charged residues characteristic of a transmembrane domain and is anchored to the cell membrane by glycosyl-phosphatidylinositol (GPI) linkage, as described in greater detail below. Although the absence of an intracellular catalytic domain precluded a direct role in transmembrane signaling, the high binding affinity and strong evolutionary sequence
20 conservation further suggested that this receptor was important for GDNF function.

Because GDNFR lacks a cytoplasmic domain, it was thought that this receptor must act in conjunction with one or more accessory molecules which play a role in transmembrane signaling. It was then discovered that transgenic mice which lack the gene for GDNF die and have no kidneys. Transgenic mice which lack the gene for
25 c-ret proto-oncogene (Schuchardt, et al., Nature, 367, 380-383, 1994) were found to have a similar phenotype. The c-ret proto-oncogene encodes a receptor tyrosine kinase (RTK) whose normal function had not yet been determined. All RTKs have a similar topology: they possess an extracellular ligand-binding domain, a transmembrane domain and a cytoplasmic segment containing the catalytic protein-tyrosine kinase
30 domain. Binding of a ligand leads to the activation of the kinase domain and phosphorylation of specific substrates in the cell that mediate intracellular signaling. The present invention involves the discovery that a soluble form of GDNFR may be used to mediate the binding of GDNF to the c-ret proto-oncogene and thereby elicit a cellular response to GDNF as well as modify its cell-type specificity.

35 Similar species, called "receptor alpha" components, provide ligand binding specificity but do not have the capacity to transduce signal on their own. Such components are found in the ciliary neurotrophic factor (CNTF) and interleukin-6 (IL-

6) receptor systems. Like GDNFR, and in contrast to IL-6 receptor, CNTF receptor binds its ligand with high affinity, has a hydrophobic C-terminus, no cytoplasmic domain, and is anchored to the cell membrane by GPI linkage (Davis et al., 1991). In order to mediate signal transduction, CNTF binds first to CNTF receptor, creating a complex which is able to bind gp130. This inactive complex then binds to LIF receptor to form the active signaling complex (Davis, et al., Science, 260, 1805-1807, 1993). As with the present invention, CNTF receptor (the ligand specific binding component) must be present for signaling to occur but it need not be membrane bound (Economides et al., Science, 270, 1351-1353, 1995).

10 As further described below, GDNFR protein may be anchored to a cell surface, or it may be provided in a soluble form. In either case, GDNFR protein forms a ligand complex with GDNF, and the ligand complex binds to cell surface receptor to effectuate intracellular signaling. Thus, a soluble form of GDNFR may be used to potentiate the action of GDNF and/or modify its cell-type specificity.

15 GDNFR is unrelated to any known receptor. There are no apparent matches in the GenBank and Washington University-Merck databases for related sequences. An expressed sequence tag (EST) found in the Washington University-Merck EST database shows 75% homology to a small portion of the coding region of GDNFR (approximately 340 nucleotides of the 521 nucleotides of sequence generated from the 5' end of the clone). This clone (GenBank accession #H12981) was isolated from an oligo-dT primed human infant brain library and cloned directionally into the Lfmid BA vector (Hillier, L. et al, unpublished data). The 3' end of the #H12981 clone has been sequenced, but it exhibits no homology to any part of the GDNFR. The appearance of homology between this #H12981 clone and GDNFR over a short region, which homology then disappears, suggests that the #H12981 clone represents an unspliced transcript, or cloning artifact rather than a bona fide cDNA transcript.

25 Thus, the present invention enables the cloning of GDNFR protein by providing a method for selecting target cells which express GDNFR. By providing a means of enriching for GDNFR encoding sequences, the present invention further provides for the purification of GDNFR protein and the direct cloning of GDNFR-encoding DNA. The present description of the GDNFR nucleic acid and amino acid sequences provides the information needed to reproduce these entities as well as a variety of GDNFR analogs. With this information, GDNFR protein products may be isolated or generated by any means known to those skilled in the art. A variety of means for the recombinant or synthetic production of GDNFR protein are disclosed.

35 As used herein, the term "GDNFR protein product" includes biologically active purified natural, synthetic or recombinant GDNFR, GDNFR analogs (i.e., GDNFR

homologs and variants involving insertion, substitution and deletion variations), and chemically modified derivatives thereof. GDNFR analogs are substantially homologous to the GDNFR amino acid sequences set forth in Figures 2 and 4 (SEQ ID NOs:2 and 4).

5 The term "biologically active", as used herein, means that the GDNFR protein product demonstrates high affinity binding to GDNF and mediates or enhances GDNF-induced signal transduction. Using the present disclosure, it is well within the ability of those of ordinary skill in the art to determine whether a GDNFR polypeptide analog has substantially the same biological activity as the GDNFR protein products
10 set forth in Figures 2 and 4.

The term "substantially homologous" amino acid sequence, as used herein, refers to an amino acid sequence sharing a degree of "similarity" or homology to the GDNFR amino acid sequences set forth in Figures 2 and 4 such that the homologous sequence has a biological activity or function similar to that described for these
15 GDNFR amino acid sequences. It will be appreciated by those skilled in the art, that a relatively large number of individual or grouped amino acid residues can be changed, positionally exchanged (e.g.s, reverse ordered or reordered) or deleted entirely in an amino acid sequence without affecting the three dimensional configuration or activity of the molecule. Such modifications are well within the ability of one skilled in the art
20 following the present disclosure. The identification and means of providing such modified sequences are described in greater detail below. It is preferable that the degree of homology of a substantially homologous protein (peptide) is equal to or in excess of 70% (i.e., a range of from 70% to 100% homology). Thus, a preferable "substantially homologous" GDNFR amino acid sequence may have a degree of
25 homology greater than or equal to 70% of the amino acid sequences set forth in SEQ ID NOs:2 and 4. More preferably the degree of homology may be equal to or in excess of 85%. Even more preferably it is equal to or in excess of 90%, or most preferably it is equal to or in excess of 95%.

The percentage of homology as described herein is calculated as the percentage
30 of amino acid residues found in one protein sequence which align with identical or similar amino acid residues in the second protein sequence. Thus, in the case of GDNFR homology, the degree of sequence homology may be determined by optimally aligning the amino acid residues of the comparison molecule to those of a reference GDNFR polypeptide, such as depicted in SEQ ID NOs: 2 and 4 or those
35 encoded by the nucleic acid sequences depicted in the Figures, to maximize matches of residues between the two sequences. It will be appreciated by those skilled in the art that such alignment may include appropriate conservative residue substitutions and will

disregard truncations and internal deletions or insertions of the comparison sequence by introducing gaps as required; see, for example Dayhoff, Atlas of Protein Sequence and Structure Vol. 5, wherein an average of three or four gaps in a length of 100 amino acids may be introduced to assist in alignment (p. 124, National Biochemical Research Foundation, Washington, D.C., 1972; the disclosure of which is hereby incorporated by reference). Once so aligned, the percentage is determined by the number of aligned residues in the comparison polypeptide divided by the total number of residues in the comparison polypeptide. It is further contemplated that the GDNFR sequences of the present invention may be used to form a portion of a fusion protein or chimeric protein which has, at least in part, GDNFR activity. The alignment and homology of such a protein would be determined using that portion of the fusion protein or chimeric protein which is related to GDNFR activity.

The sources of such substantially homologous GDNFR proteins include the GDNFR proteins of other mammals which are expected to have a high degree of homology to the human GDNFR protein. For example, the degree of homology between the rat and human GDNFR proteins disclosed herein is about 93%. Substantially homologous GDNFR proteins may be isolated from such mammals by virtue of cross-reactivity with antibodies to the GDNFR amino acid sequences of SEQ ID NOs: 2 and 4. Alternatively, they may be expressed by nucleic acid sequences which are isolated through hybridization with the gene or with segments of the gene encoding the GDNFR of SEQ ID NOs 2 and 4 or which hybridize to a complementary sequence of the nucleic acid sequences illustrated in SEQ ID NOs: 2 and 4. Suitable hybridization conditions are described in further detail below.

The novel GDNFR protein products are typically isolated and purified to form GDNFR protein products which are substantially free of unwanted substances that would detract from the use of the present polypeptides for an intended purpose. For example, preferred GDNFR protein products may be substantially free from the presence of other human (e.g., non-GDNFR) proteinaceous materials or pathological agents. Preferably, the GDNFR protein products are about 80% free of other proteins which may be present due to the production technique used in the manufacture of the GDNFR protein product. More preferably, the GDNFR protein products are about 90% free of other proteins, particularly preferably, about 95% free of other proteins, and most preferably about >98% free of other proteins. In addition, the present invention furnishes the unique advantage of providing polynucleotide sequences for the manufacture of homogeneous GDNFR proteins.

A variety of GDNFR variants are contemplated, including addition, deletion and substitution variants. For example, a series of deletion variants may be made by

removing one or more amino acid residues from the amino and/or carboxy termini of the GDNFR protein. Using rules for the prediction of signal peptide cleavage as described by von Heijne (von Heijne, *Nucleic Acids Research*, 14, 4683-4690, 1986), the first amino acid residue of the GDNFR protein which might be involved in GDNF binding is Ser¹⁸, as depicted in the full length amino acid sequence of human GDNFR in Figure 2 (SEQ ID NO:2). Amino acid residues Met¹ through Ser¹⁸ are in the amino-terminal hydrophobic region that is likely to be part of a signal peptide sequence, and therefore, not be included in the mature form of the receptor protein. Similarly, the last amino acid residue of the GDNFR protein which is likely to be necessary for GDNF binding is Ser⁴⁴⁶. Amino acid residues Leu⁴⁴⁷ through Ser⁴⁶⁵ are in the carboxy-terminal hydrophobic region that is involved in the GPI linkage of the protein to the cell surface. Thus, it is contemplated that any or all of the residues from Met¹ through Ser¹⁸ and/or Leu⁴⁴⁷ through Ser⁴⁶⁵ (as depicted in Figure 2 (SEQ ID NO:2) may be removed from the protein without affecting GDNF binding to the GDNFR protein, thereby leaving a "core" sequence of Ala¹⁹ through Pro⁴⁴⁶. Using known analysis techniques, it is further contemplated that N-terminal truncations may include the removal of one or more amino acid residues up to and including Gly²⁴. Thus, GDNFR truncation analogs also may include the deletion of one or more amino acid residues from either or both termini such that an amino acid sequence of Asp²⁵ through Pro⁴⁴⁶ or Leu⁴⁴⁷ forms the basis for a core molecule. Additional GDNFR analogs are contemplated as involving amino acid residues Ser¹⁸ through Pro⁴⁴⁹ as depicted in the GDNFR amino acid sequence of Figure 4 (SEQ ID NO:4), i.e., deleting one or more amino acid residues from either or both termini involving the hydrophobic regions depicted as amino acid residues Met¹ through Ser¹⁸ and/or Pro⁴⁴⁹ through Ser⁴⁶⁸.

In addition, it is contemplated that one or more amino acid residues may be removed from either or both of the amino and carboxy termini until the first and last cysteine residues in the full length sequence are reached. It is advantageous to retain the cysteine residues for the proper intramolecular binding of the GDNFR protein. As depicted in the full length amino acid sequence of human GDNFR in Figure 2 (SEQ ID NO:2), any or all of amino acid residues from Met¹ to Asp²⁸ may be removed from the amino terminal without removing the first cysteine residue which appears as Cys²⁹. Similarly, any or all of amino acid residues from Gly⁴⁴³ to Ser⁴⁶⁵ may be removed from the carboxy terminal without removing the last cysteine residue which appears as Cys⁴⁴². Other GDNFR analogs may be made using amino acid residues Cys²⁹ through Cys⁴⁴³ as depicted in the GDNFR amino acid sequence of Figure 4 (SEQ ID NO:4), i.e., deleting all or part of the terminal regions depicted as amino acid

residues Met¹ through Asp²⁸ and/or Ser⁴⁴⁴ through Ser⁴⁶⁸

It will be appreciated by those skilled in the art that, for the same reasons, it is contemplated that these identified amino acid residues may be replaced, rather than deleted, without affecting the function of the GDNFR protein. Alternatively, these identified amino acid residues may be modified by intra-residue insertions or terminal additions without affecting the function of the GDNFR protein. In yet another embodiment, a combination of one or more deletions, substitutions or additions may be made.

The present GDNFR proteins or nucleic acids may be used for methods of treatment, or for methods of manufacturing medicaments for treatment. Such treatment includes conditions characterized by excessive production of GDNFR protein, wherein the present GDNFRs, particularly in soluble form, may be used to complex to and therefore inactivate such excessive GDNF protein. This treatment may be accomplished by preparing soluble receptor (e.g., use of the GDNF binding domain) or by preparation of a population of cells containing such GDNFR, and transplanting such cells into the individual in need thereof. The present GDNFR protein products may also be used for treatment of those having defective GDNF receptors. For example, one may treat an individual having defective GDNFRs by preparation and delivery of a soluble receptor, or by preparation of a population of cells containing such non-defective GDNFR and transplanting such cells into an individual. Or, an individual may have an inadequate number of GDNF receptors, and cells containing such receptors may be transplanted in order to increase the number of GDNF receptors available to an individual. Such compositions may be used in conjunction with the delivery of GDNF. It is also contemplated GDNFR protein products may be used in the treatment of conditions responsive to the activation of the c-ret receptor tyrosine kinase.

In yet another aspect of the present invention, a further advantage to the novel compositions is the use of GDNFR to stabilize GDNF protein pharmaceutical compositions. In another aspect of the present invention, a GDNFR may be used to screen compounds for antagonist activity.

Other aspects and advantages of the present invention will be apparent to those skilled in the art. For example, additional uses include new assay systems, transgenic animals and antibody production.

Study Models

The present invention provides for assay systems in which GDNF activity or

activities similar to GDNF activity resulting from exposure to a peptide or non-peptide compound may be detected by measuring an elicited physiological response in a cell or cell line which expresses the GDNFR molecules of the present invention. A physiological response may comprise any of the biological effects of GDNF, including but not limited to, dopamine uptake, extension of neurites, increased cell survival or growth, as well as the transcriptional activation of certain nucleic acid sequences (e.g. promoter/enhancer elements as well as structural genes), GDNF-related processing, translation, or phosphorylation, and the induction of secondary processes in response to processes directly or indirectly induced by GDNF, to name but a few.

For example, a model system may be created which may be used to study the effects of excess GDNF activity. In such a system, the response of a cell to GDNF may be increased by engineering an increased number of GDNFRs on the cells of the model system relative to cells which have not been so modified. A system may also be developed to selectively provide an increased number of GDNFRs on cells which normally express GDNFRs. In order to ensure expression of GDNFR, the GDNFR gene may be placed under the control of a suitable promoter sequence. It may be desirable to put the GDNFR gene under the control of a constitutive and/or tissue specific promoter (including but not limited to the CNS neuron specific enolase, neurofilament, and tyrosine hydroxylase promoter), an inducible promoter (such as the metallothionein promoter), the UV activated promoter in the human immunodeficiency virus long terminal repeat (Valeri et al., 1988, Nature 333:78-81), or the CMV promoter (as contained in pCMX, *infra*) or a developmentally regulated promoter.

By increasing the number of cellular GDNFRs, the response to endogenous GDNF may be increased. If the model system contains little or no GDNF, GDNF may be added to the system. It may also be desirable to add additional GDNF to the model system in order to evaluate the effects of excess GDNF activity. Over expressing GDNF (or secreted GDNF) may be one method for studying the effects of elevated levels of GDNF on cells already expressing GDNFR.

30

GDNFR Therapies

In another aspect, certain conditions may benefit from an increase in GDNF responsiveness. It may, therefore, be beneficial to increase the number or binding affinity of GDNFRs in patients suffering from conditions responsive to GDNF therapy. This could be achieved through gene therapy, whereby selective expression of recombinant GDNFR in appropriate cells is achieved, for example, by using GDNFR genes controlled by tissue specific or inducible promoters or by producing

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localized infection with replication defective viruses carrying a recombinant GDNFR gene.

It is envisioned that conditions which will benefit from GDNFR or combined GDNF/GDNFR delivery include, but are not limited to, motor neuron disorders including amyotrophic lateral sclerosis, neurological disorders associated with diabetes, Parkinson's disease, Alzheimer's disease, and Huntington's chorea. Additional indications for the use of GDNFR or combined GDNF/GDNFR delivery are described above and further include the treatment of: glaucoma or other diseases and conditions involving retinal ganglion cell degeneration; sensory neuropathy caused by injury to, insults to, or degeneration of, sensory neurons; pathological conditions, such as inherited retinal degenerations and age, disease or injury-related retinopathies, in which photoreceptor degeneration occurs and is responsible for vision loss; and injury or degeneration of inner ear sensory cells, such as hair cells and auditory neurons for preventing and/or treating hearing loss due to variety of causes.

Transgenic Animals

In yet another aspect, a recombinant GDNFR gene may be used to inactivate or "knock out" the endogenous gene (e.g., by homologous recombination) and thereby create a GDNFR deficient cell, tissue, or animal. For example, a recombinant GDNFR gene may be engineered to contain an insertional mutation which inactivates GDNFR. Such a construct, under the control of a suitable promoter, may be introduced into a cell, such as an embryonic stem cell, by any conventional technique including transfection, transduction, injection, etc. Cells containing the construct may then be selected, for example by G418 resistance. Cells which lack an intact GDNFR gene are then identified (e. g., by Southern blotting or Northern blotting or assay of expression). Cells lacking an intact GDNFR gene may then be fused to early embryo cells to generate transgenic animals deficient in GDNFR. A comparison of such an animal with an animal not expressing endogenous GDNF would reveal that either the two phenotypes match completely or that they do not, implying the presence of additional GDNF-like factors or receptors. Such an animal may be used to define specific neuronal populations, or other in vivo processes, normally dependent upon GDNF. Thus, these populations or processes may be expected to be effected if the animal did not express GDNFR, and therefore, could not respond to GDNF.

Diagnostic Applications

According to the present invention, GDNFR probes may be used to identify cells and tissues which are responsive to GDNF in normal or diseased states. The

present invention provides for methods for identifying cells which are responsive to GDNF by detecting GDNFR expression in such cells. GDNFR expression may be evidenced by transcription of GDNFR mRNA or production of GDNFR protein. GDNFR expression may be detected using probes which identify GDNFR nucleic acid or protein or by detecting "tag" sequences artificially added to the GDNFR protein.

One variety of probe which may be used to detect GDNFR expression is a nucleic acid probe, which may be used to detect GDNFR-encoding RNA by any method known in the art, including, but not limited to, in situ hybridization, Northern blot analysis, or PCR related techniques. Nucleic acid products of the invention may be labeled with detectable markers (such as radiolabels and non-isotopic labels such as biotin) and employed in hybridization processes to locate the human GDNFR gene position and/or the position of any related gene family in a chromosomal map. They may also be used for identifying human GDNFR gene disorders at the DNA level and used as gene markers for identifying neighboring genes and their disorders.

Contemplated herein are kits containing such labeled materials.

Polypeptide products of the invention may be "labeled" by association with a detectable marker substance or label (e.g., a radioactive isotope, a fluorescent or chemiluminescent chemical, an enzyme or other label available to one skilled in the art) to provide reagents useful in detection and quantification of GDNF in solid tissue and fluid samples such as blood or urine. Such products may also be used in detecting cells and tissues which are responsive to GDNF in normal or diseased states.

Another possible assay for detecting the presence of GDNF in a test sample or screening for the presence of a GDNF-like molecule involves contacting the test sample with a GDNFR peptide immobilized on a solid phase, thereby producing GDNFR-bound GDNF. The GDNFR-bound GDNF may optionally be contacted with a detection reagent, such as a labeled antibody specific for GDNF, thereby forming a detectable product. Such assays may be developed in the form of assay devices for analyzing a test sample. In a basic form, such devices include a solid phase containing or coated with GDNFR. A method for analyzing a test sample for the presence of GDNF may involve contacting the sample to an assay reagent comprising GDNFR protein, wherein said GDNFR protein reacts with GDNF present in the test sample and produces a detectable reaction product indicative of the presence of GDNF.

The assay reagents provided herein may also be embodied as part of a kit or article of manufacture. Contemplated is an article of manufacture comprising a packaging material and one or more preparations of the presently provided nucleic acid or amino acid sequences. Such packaging material will comprise a label indicating that

the preparation is useful for detecting GDNF, GDNFR or GDNFR defects in a biological sample. As such, the kit may optionally include materials to carry out such testing, such as reagents useful for performing protein analysis, DNA or RNA hybridization analysis, or PCR analysis on blood, urine, or tissue samples.

5

Anti-GDNFR Antibody

According to the present invention, GDNFR protein, or fragments or derivatives thereof, may be used as an immunogen to generate anti-GDNFR antibodies. To further improve the likelihood of producing an anti-GDNFR immune response, the amino acid sequence of GDNFR may be analyzed in order to identify portions of the molecule which may be associated with increased immunogenicity. For example, the amino acid sequence may be subjected to computer analysis to identify surface epitopes which present computer-generated plots of hydrophilicity, surface probability, flexibility, antigenic index, amphiphilic helix, amphiphilic sheet, and secondary structure of GDNFR. Alternatively, the amino acid sequences of GDNFR from different species could be compared, and relatively non-homologous regions identified; these non-homologous regions would be more likely to be immunogenic across various species.

Also comprehended are polypeptide fragments duplicating only a part of the continuous amino acid sequence or secondary conformations within GDNFR, which fragments may possess one activity of mammalian GDNFR (e.g., immunological activity) and not others (e.g., GDNF protein binding activity). Thus, the production of antibodies can include the production of anti-peptide antibodies. The following exemplary peptides were synthesized using GDNFR sequences:

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TABLE 1
GDNFR Peptides

SJP-6	H ₂ N-QSCSTKYRTL-COOH	human GDNFR, AA 40-49 (SEQ ID NO:25)
SJP-7	H ₂ N-CKRGMKKEKN-COOH	human GDNFR, AA 89-98 (SEQ ID NO:26)
SJP-8	H ₂ N-LLEDSPYEPV-COOH	human GDNFR, AA 115-124 (SEQ ID NO:27)
SJP-9	H ₂ N-CSYEERERPN-COOH	rat GDNFR, AA 233-242 (SEQ ID NO:28)
SJP-10	H ₂ N-PAPPVQTTTATTTT-COOH	rat GDNFR, AA 356-369 (SEQ ID NO:29)

Peptides SJP-6, 7, and 8 are identical in rat and human GDNFR. Peptides SJP-9 and 10 are derived from the rat sequence and are each one amino acid different from human. Both polyclonal and monoclonal antibodies may be made by methods known in the art using these peptides or other portions of GDNFR.

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Monoclonal antibodies directed against GDNFR may be prepared by any known technique which provides for the production of antibody molecules by continuous cell lines in culture. For example, the hybridoma technique originally developed by Kohler and Milstein to produce monoclonal antibodies (Nature, 5 256:495-497, 1975), as well as the trioma technique, the human B-cell hybridoma technique (Kozbor et al., Immunology Today 4:72, 1983), the EBV-hybridoma technique (Cole et al., in "Monoclonal Antibodies and Cancer Therapy," Alan R. Liss, Inc. pp. 77-96, 1985), and the like, may be used.

Human monoclonal antibodies or chimeric human-mouse (or other species) 10 monoclonal antibodies also may be prepared for therapeutic use and may be made by any of numerous techniques known in the art (e.g., Teng et al., Proc. Natl. Acad. Sci. U.S.A., 80:7308-7312, 1983; Kozbor et al., Immunology Today, 4:72-79, 1983; Olsson et al., Meth. Enzymol., 92:3-16, 1982). Chimeric antibody molecules may be prepared containing a mouse antigen-binding domain with human constant regions 15 (Morrison et al., Proc. Natl. Acad. Sci. U.S.A., 81:6851, 1984; Takeda et al., Nature, 314:452, 1985).

Various procedures known in the art also may be used for the production of polyclonal antibodies. For the production of antibody, various host animals including, but not limited to, rabbits, mice, rats, etc., can be immunized by injection with 20 GDNFR protein, or a fragment or derivative thereof. Various adjuvants may be used to increase the immunological response, depending on the host species selected. Useful adjuvants include, but are not limited to, Freund's (complete and incomplete), mineral gels such as aluminum hydroxide, surface active substances such as lysolecithin, pluronic polyols, polyanions, peptides, oil emulsions, keyhole limpet 25 hemocyanins, dinitrophenol, and human adjuvants such as BCG (Bacille Calmette-Guerin) and Corynebacterium parvum.

A molecular clone of an antibody to a GDNFR epitope also may be prepared by known techniques. Recombinant DNA methodology (see e.g., Maniatis et al., Molecular Cloning, A Laboratory Manual, Cold Spring Harbor Laboratory, Cold 30 Spring Harbor, N.Y., 1982) may be used to construct nucleic acid sequences which encode a monoclonal antibody molecule, or antigen binding region thereof.

Antibody molecules may be purified by known techniques, e.g., immunoabsorption or immunoaffinity chromatography, chromatographic methods such as high performance liquid chromatography, or a combination thereof, etc. The 35 present invention provides for antibody molecules as well as fragments of such antibody molecules. Antibody fragments which contain the idiotype of the molecule can be generated by known techniques. For example, such fragments include but are

not limited to: the F(ab')₂ fragment which can be produced by pepsin digestion of the antibody molecule; the Fab' fragments which can be generated by reducing the disulfide bridges of the F(ab')₂ fragment, and the Fab fragments which can be generated by treating the antibody molecule with papain and a reducing agent.

- 5 Such selective binding molecules may themselves be alternatives to GDNFR protein, and may be formulated as a pharmaceutical composition.

Recombinant Expression of GDNFR Protein

- 10 The present invention provides various polynucleotides encoding GDNFR proteins. The expression product or a derivative thereof is characterized by the ability to bind to GDNF specifically and with high affinity so that further interactions with signaling molecules can occur, thereby providing or enhancing GDNF activity such as increasing dopamine uptake by dopaminergic cells. The polynucleotides may also be used in cell therapy or gene therapy applications.

- 15 According to the present invention, novel GDNFR protein and DNA sequences coding for all or part of such receptors are provided. Novel nucleic acid sequences of the invention include sequences useful in securing expression in procaryotic or eucaryotic host cells of polypeptide products having at least a part of the primary structural conformation and one or more of the biological properties of recombinant human GDNFR. The nucleic acids may be purified and isolated, so that the desired coding region is useful to produce the present polypeptides. Alternatively, the nucleic acid sequence may be used for diagnostic purposes, as described more fully below. Exemplary DNA sequences of the present invention comprise nucleic acid sequences encoding the GDNFR amino acid sequences depicted in Figures 2 and 4 and set forth in SEQ. ID NOs:2 and 4. In addition, DNA sequences disclosed by the present invention specifically comprise: (a) any of the DNA sequences depicted in Figures 1 and 3 (and complementary strands); (b) a DNA sequence which hybridizes (under hybridization conditions disclosed in the cDNA library screening section below, or equivalent conditions or more stringent conditions) to the DNA sequence in subpart (a) or to fragments thereof; and (c) a DNA sequence which, but for the degeneracy of the genetic code, would hybridize to the DNA sequence in subpart (a). Specifically
25 comprehended in parts (b) and (c) are genomic DNA sequences encoding allelic variant forms of human GDNFR and/or encoding GDNFR from other mammalian species, and manufactured DNA sequences encoding GDNFR, fragments of GDNFR, and analogs of GDNFR which DNA sequences may incorporate codons facilitating
30 transcription and translation of messenger RNA in microbial hosts. Such manufactured sequences may readily be constructed according to the methods known
- 35

in the art as well as the methods described herein.

Recombinant expression techniques, conducted in accordance with the descriptions set forth herein or other known methods, may be used to produce these polynucleotides and express the various GDNFR proteins. For example, by inserting
5 a nucleic acid sequence which encodes a GDNFR protein into an appropriate vector, one skilled in the art can readily produce large quantities of the desired nucleotide sequence. The sequences can then be used to generate detection probes or amplification primers. Alternatively, a polynucleotide encoding a GDNFR protein can be inserted into an expression vector. By introducing the expression vector into an
10 appropriate host, the desired GDNFR protein may be produced in large amounts.

As further described herein, there are numerous host/vector systems available for the propagation of nucleic acid sequences and/or the production of GDNFR proteins. These include, but are not limited to, plasmid, viral and insertional vectors, and prokaryotic and eukaryotic hosts. One skilled in the art can adapt a host/vector
15 system which is capable of propagating or expressing heterologous DNA to produce or express the sequences of the present invention.

By means of such recombinant techniques, the GDNFR proteins of the present invention are readily produced in commercial quantities with greater purity. Furthermore, it will be appreciated by those skilled in the art that, in view of the
20 present disclosure, the novel nucleic acid sequences include degenerate nucleic acid sequences encoding the GDNFR proteins specifically set forth in the Figures, sequences encoding variants of GDNFR proteins, and those nucleic acid sequences which hybridize, preferably under stringent hybridization conditions, to complements of these nucleic acid sequences (see, Maniatis et. al., Molecular Cloning (A Laboratory
25 Manual); Cold Spring Harbor Laboratory, pages 387 to 389, 1982.) Exemplary stringent hybridization conditions are hybridization in 4 x SSC at 62-67°C, followed by washing in 0.1 x SSC at 62-67°C for approximately an hour. Alternatively, exemplary stringent hybridization conditions are hybridization in 45-55% formamide, 4 x SSC at 40-45°C. DNA sequences which hybridize to the complementary
30 sequences for GDNFR protein under relaxed hybridization conditions and which encode a GDNFR protein of the present invention are also included herein. Examples of such relaxed stringency hybridization conditions are 4 x SSC at 45-55°C or hybridization with 30-40% formamide at 40-45°C.

Preparation of Polynucleotides Encoding GDNFR

Based upon the disclosure of the present invention, a nucleic acid sequence encoding a full length GDNFR polypeptide or a fragment thereof may readily be prepared or obtained in a variety of ways, including, without limitation, chemical synthesis, cDNA or genomic library screening, expression library screening, and/or PCR amplification of cDNA. These methods and others useful for preparing nucleic acid sequences are known in the art and are set forth, for example, by Sambrook et al. (Molecular Cloning: A Laboratory Manual, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, NY, 1989), by Ausubel et al., eds (Current Protocols in Molecular Biology, Current Protocols Press, 1994), and by Berger and Kimmel (Methods in Enzymology: Guide to Molecular Cloning Techniques, vol. 152, Academic Press, Inc., San Diego, CA, 1987). Preferred nucleic acid sequences encoding GDNFR are mammalian sequences.

Chemical synthesis of a nucleic acid sequence which encodes a GDNFR protein can also be accomplished using methods known in the art, such as those set forth by Engels et al. (Angew. Chem. Intl. Ed., 28:716-734, 1989). These methods include, inter alia, the phosphotriester, phosphoramidite and H-phosphonate methods of nucleic acid sequence synthesis. A preferred method for such chemical synthesis is polymer-supported synthesis using standard phosphoramidite chemistry. Typically, the DNA encoding the desired polypeptide will be several hundred base pairs (bp) or nucleotides in length. Nucleic acid sequences larger than about 100 nucleotides can be synthesized as several fragments using these methods. The fragments can then be ligated together to form a sequence for the expression of a full length GDNFR polypeptide or a portion thereof.

Alternatively, a suitable nucleic acid sequence may be obtained by screening an appropriate cDNA library (i.e., a library prepared from one or more tissue source(s) believed to express the protein) or a genomic library (a library prepared from total genomic DNA). The source of the cDNA library is typically a tissue that is believed to express GDNFR in reasonable quantities. Typically, the source of the genomic library is any tissue or tissues from a mammalian species believed to harbor a gene encoding GDNFR. The library can be screened for the presence of the GDNFR cDNA/gene using one or more nucleic acid probes (such as oligonucleotides, cDNA or genomic DNA fragments based upon the presently disclosed sequences) that will hybridize selectively with GDNFR cDNA(s) or gene(s) present in the library. The probes typically used for such library screening usually encode a small region of the GDNFR nucleic acid sequence from the same or a similar species as the species from which the library was prepared. Alternatively, the probes may be degenerate, as discussed

herein.

Library screening is typically accomplished by annealing the oligonucleotide probe or cDNA to the clones in the library under conditions of stringency that prevent non-specific binding but permit binding (hybridization) of those clones that have a significant level of homology with the probe or primer. Typical hybridization and washing stringency conditions depend in part on the size (i.e., number of nucleotides in length) of the cDNA or oligonucleotide probe, and whether the probe is degenerate. The probability of obtaining a clone(s) is also considered in designing the hybridization solution (e.g., whether a cDNA or genomic library is being screened; if it is a cDNA library, the probability that the cDNA of interest is present at a high level).

Where DNA fragments (such as cDNAs) are used as probes, typical hybridization conditions include those as set forth in Ausubel et al., eds., supra. After hybridization, the blot containing the library is washed at a suitable stringency, depending on several factors such as probe size, expected homology of probe to clone, type of library being screened, number of clones being screened, and the like. Examples of stringent washing solutions (which are usually low in ionic strength and are used at relatively high temperatures) are as follows. One such stringent wash is 0.015 M NaCl, 0.005 M NaCitrate and 0.1% SDS at 55-65°C. Another such stringent buffer is 1 mM Na₂EDTA, 40 mM NaHPO₄, pH 7.2, and 1% SDS at about 40-50°C. One other stringent wash is 0.2 X SSC and 0.1% SDS at about 50-65°C.

There are also exemplary protocols for stringent washing conditions where oligonucleotide probes are used to screen cDNA or genomic libraries. For example, a first protocol uses 6 X SSC with 0.05 percent sodium pyrophosphate at a temperature of between about 35 and 62°C, depending on the length of the probe. For example, 14 base probes are washed at 35-40°C, 17 base probes at 45-50°C, 20 base probes at 52-57°C, and 23 base probes at 57-63°C. The temperature can be increased 2-3°C where the background non-specific binding appears high. A second protocol uses tetramethylammonium chloride (TMAC) for washing. One such stringent washing solution is 3 M TMAC, 50 mM Tris-HCl, pH 8.0, and 0.2% SDS.

Another suitable method for obtaining a nucleic acid sequence encoding a GDNFR protein is by polymerase chain reaction (PCR). In this method, poly(A)+RNA or total RNA is extracted from a tissue that expresses GDNFR. A cDNA is then prepared from the RNA using the enzyme reverse transcriptase (i.e., RT-PCR). Two primers, typically complementary to two separate regions of the GDNFR cDNA (oligonucleotides), are then added to the cDNA along with a polymerase such as Taq polymerase, and the polymerase amplifies the cDNA region

between the two primers.

Where the method of choice for preparing the nucleic acid sequence encoding the desired GDNFR protein requires the use of oligonucleotide primers or probes (e.g., PCR, cDNA or genomic library screening), the oligonucleotide sequences
5 selected as probes or primers should be of adequate length and sufficiently unambiguous so as to minimize the amount of non-specific binding that will occur during library screening or PCR amplification. The actual sequence of the probes or primers is usually based on conserved or highly homologous sequences or regions from the same or a similar gene from another organism, such as the rat nucleic acid
10 sequence involved in the present invention. Optionally, the probes or primers can be fully or partially degenerate, i.e., contain a mixture of probes/primers, all encoding the same amino acid sequence, but using different codons to do so. An alternative to preparing degenerate probes is to place an inosine in some or all of those codon positions that vary by species. The oligonucleotide probes or primers may be prepared
15 by chemical synthesis methods for DNA as described above.

GDNFR proteins based on these nucleic acid sequences encoding GDNFR, as well as mutant or variant sequences thereof, are also contemplated as within the scope of the present invention. Mutant or variant sequences include those sequences containing one or more nucleotide substitutions, deletions, and/or insertions as
20 compared to the wild type sequence and that results in the expression of amino acid sequence variations as compared to the wild type amino acid sequence. In some cases, naturally occurring GDNFR amino acid mutants or variants may exist, due to the existence of natural allelic variation. GDNFR proteins based on such naturally occurring mutants or variants are also within the scope of the present invention.
25 Preparation of synthetic mutant sequences is also well known in the art, and is described for example in Wells et al. (Gene, 34:315, 1985) and in Sambrook et al., supra.

In some cases, it may be desirable to prepare nucleic acid and/or amino acid variants of naturally occurring GDNFR. Nucleic acid variants (wherein one or more
30 nucleotides are designed to differ from the wild-type or naturally occurring GDNFR) may be produced using site directed mutagenesis or PCR amplification where the primer(s) have the desired point mutations (see Sambrook et al., supra, and Ausubel et al., supra, for descriptions of mutagenesis techniques). Chemical synthesis using methods described by Engels et al., supra, may also be used to prepare such variants.
35 Other methods known to the skilled artisan may be used as well. Preferred nucleic acid variants are those containing nucleotide substitutions accounting for codon preference in the host cell that is to be used to recombinantly produce GDNFR. Other

preferred variants are those encoding conservative amino acid changes (e.g., wherein the charge or polarity of the naturally occurring amino acid side chain is not altered substantially by substitution with a different amino acid) as compared to wild type, and/or those designed to either generate a novel glycosylation and/or phosphorylation site(s) on GDNFR, or those designed to delete an existing glycosylation and/or phosphorylation site(s) on GDNFR.

Vectors

The cDNA or genomic DNA encoding the desired GDNFR protein is inserted into a vector for further cloning (amplification of the DNA) or for expression. Suitable vectors are commercially available, or the vector may be specially constructed. Possible vectors include, but are not limited to, cosmids, plasmids or modified viruses, but the vector system must be compatible with the selected host cell. Such vectors include, but are not limited to, bacteriophages such as lambda derivatives, or plasmids such as pBR322, pUC, or Bluescript[®] plasmid derivatives (Stratagene, La Jolla CA). The recombinant molecules can be introduced into host cells via transformation, transfection, infection, electroporation, or other known techniques.

For example, the GDNFR-encoding nucleic acid sequence is inserted into a cloning vector which is used to transform, transfect, or infect appropriate host cells so that many copies of the nucleic acid sequence are generated. This can be accomplished by ligating a DNA fragment into a cloning vector which has complementary cohesive termini. If the complementary restriction sites used to fragment the DNA are not present in the cloning vector, the ends of the DNA molecules may be enzymatically modified. It also may prove advantageous to incorporate restriction endonuclease cleavage sites into the oligonucleotide primers used in polymerase chain reaction to facilitate insertion of the resulting nucleic acid sequence into vectors. Alternatively, any site desired may be produced by ligating nucleotide sequences (linkers) onto the DNA termini; these ligated linkers may comprise specific chemically synthesized oligonucleotides encoding restriction endonuclease recognition sequences. In an alternative method, the cleaved vector and GDNFR-encoding nucleic acid sequence may be modified by homopolymeric tailing. In specific embodiments, transformation of host cells with recombinant DNA molecules that incorporate an isolated GDNFR gene, cDNA, or synthesized DNA sequence enables generation of multiple copies of the gene. Thus, the GDNFR-encoding nucleic acid sequence may be obtained in large quantities by growing transformants, isolating the recombinant DNA molecules from the transformants and, when necessary, retrieving the inserted gene from the isolated recombinant DNA.

The selection or construction of the appropriate vector will depend on 1) whether it is to be used for DNA amplification or for DNA expression, 2) the size of the DNA to be inserted into the vector, and 3) the host cell (e.g., mammalian, insect, yeast, fungal, plant or bacterial cells) to be transformed with the vector. Each vector contains various components depending on its function (amplification of DNA or expression of DNA) and its compatibility with the intended host cell. For DNA expression, the vector components may include, but are not limited to, one or more of the following: a signal sequence, an origin of replication, one or more selection or marker genes, enhancer elements, promoters, a transcription termination sequence, and the like. These components may be obtained from natural sources or synthesized by known procedures. The vectors of the present invention involve a nucleic acid sequence which encodes the GDNFR protein of interest operatively linked to one or more amplification, expression control, regulatory or similar operational elements capable of directing, controlling or otherwise effecting the amplification or expression of the GDNFR-encoding nucleic acid sequence in the selected host cell.

Expression vectors containing GDNFR nucleic acid sequence inserts can be identified by three general approaches: (a) DNA-DNA hybridization; (b) the presence or absence of "marker" gene functions, and (c) the expression of inserted sequences. In the first approach, the presence of a foreign nucleic acid sequence inserted in an expression vector can be detected by DNA-DNA hybridization using probes comprising sequences that are homologous to an inserted GDNFR-encoding nucleic acid sequence. In the second approach, the recombinant vector/host system can be identified and selected based upon the presence or absence of certain "marker" gene functions (e.g., thymidine kinase activity, resistance to antibiotics, transformation phenotype, occlusion body formation in baculovirus, etc.) caused by the insertion of a foreign nucleic acid sequence into the vector. For example, if a GDNFR-encoding nucleic acid sequence is inserted within the marker gene sequence of the vector, recombinants containing the GDNFR insert can be identified by the absence of the marker gene function. In the third approach, recombinant expression vectors can be identified by detecting the foreign protein product expressed by the recombinant nucleic acid sequence. Such assays can be based on the physical or functional properties of the expressed GDNFR protein product, for example, by binding of the GDNFR protein to GDNF or to an antibody which directly recognizes GDNFR.

35 Signal Sequence

The signal sequence may be a component of the vector, or it may be a part of GDNFR DNA that is inserted into the vector. The native GDNFR DNA encodes a

signal sequence at the amino terminus of the protein that is cleaved during post-translational processing of the protein to form the mature GDNFR protein. Included within the scope of this invention are GDNFR polynucleotides with the native signal sequence as well as GDNFR polynucleotides wherein the native signal sequence is deleted and replaced with a heterologous signal sequence. The heterologous signal sequence selected should be one that is recognized and processed, i.e., cleaved by a signal peptidase, by the host cell. For prokaryotic host cells that do not recognize and process the native GDNFR signal sequence, the signal sequence is substituted by a prokaryotic signal sequence selected, for example, from the group of the alkaline phosphatase, penicillinase, or heat-stable enterotoxin II leaders. For yeast secretion, the native GDNFR signal sequence may be substituted by the yeast invertase, alpha factor, or acid phosphatase leaders. In mammalian cell expression the native signal sequence is satisfactory, although other mammalian signal sequences may be suitable.

15 Origin of Replication

Expression and cloning vectors generally include a nucleic acid sequence that enables the vector to replicate in one or more selected host cells. In cloning vectors, this sequence is typically one that enables the vector to replicate independently of the host chromosomal DNA, and includes origins of replication or autonomously replicating sequences. Such sequences are well known for a variety of bacteria, yeasts, and viruses. The origin of replication from the plasmid pBR322 is suitable for most Gram-negative bacteria and various origins (e.g., SV40, polyoma, adenovirus, VSV or BPV) are useful for cloning vectors in mammalian cells. Generally, the origin of replication component is not needed for mammalian expression vectors (for example, the SV40 origin is often used only because it contains the early promoter).

Selection Gene

The expression and cloning vectors may contain a selection gene. This gene encodes a "marker" protein necessary for the survival or growth of the transformed host cells when grown in a selective culture medium. Host cells that were not transformed with the vector will not contain the selection gene, and therefore, they will not survive in the culture medium. Typical selection genes encode proteins that (a) confer resistance to antibiotics or other toxins, e.g., ampicillin, neomycin, methotrexate, or tetracycline; (b) complement auxotrophic deficiencies; or (c) supply critical nutrients not available from the culture medium.

Other selection genes may be used to amplify the gene which will be expressed. Amplification is the process wherein genes which are in greater demand

for the production of a protein critical for growth are reiterated in tandem within the chromosomes of successive generations of recombinant cells. Examples of suitable selectable markers for mammalian cells include dihydrofolate reductase (DHFR) and thymidine kinase. The mammalian cell transformants are placed under selection
5 pressure which only the transformants are uniquely adapted to survive by virtue of the marker present in the vector. Selection pressure is imposed by culturing the transformed cells under conditions in which the concentration of selection agent in the medium is successively changed, thereby leading to amplification of both the selection gene and the DNA that encodes GDNFR. As a result, increased quantities of GDNFR
10 are synthesized from the amplified DNA.

For example, cells transformed with the DHFR selection gene are first identified by culturing all of the transformants in a culture medium that contains methotrexate, a competitive antagonist of DHFR. An appropriate host cell when wild-type DHFR is used is the Chinese hamster ovary cell line deficient in DHFR activity
15 (see, for example, Urlaub and Chasin, Proc. Natl. Acad. Sci., U.S.A., 77(7): 4216-4220, 1980). The transformed cells are then exposed to increased levels of methotrexate. This leads to the synthesis of multiple copies of the DHFR gene, and, concomitantly, multiple copies of other DNA present in the expression vector, such as the DNA encoding a GDNFR protein.

20

Promoter

The expression and cloning vectors of the present invention will typically contain a promoter that is recognized by the host organism and operably linked to the nucleic acid sequence encoding the GDNFR protein. Promoters are untranslated
25 sequences located upstream (5') to the start codon of a structural gene (generally within about 100 to 1000 bp) that control the transcription and translation of a particular nucleic acid sequence, such as that encoding GDNFR. Promoters are conventionally grouped into one of two classes, inducible promoters and constitutive promoters. Inducible promoters initiate increased levels of transcription from DNA
30 under their control in response to some change in culture conditions, such as the presence or absence of a nutrient or a change in temperature. A large number of promoters, recognized by a variety of potential host cells, are well known. These promoters are operably linked to the DNA encoding GDNFR by removing the promoter from the source DNA by restriction enzyme digestion and inserting the
35 desired promoter sequence into the vector. The native GDNFR promoter sequence may be used to direct amplification and/or expression of GDNFR DNA. A heterologous promoter is preferred, however, if it permits greater transcription and

higher yields of the expressed protein as compared to the native promoter, and if it is compatible with the host cell system that has been selected for use.

Promoters suitable for use with prokaryotic hosts include the beta-lactamase and lactose promoter systems; alkaline phosphatase, a tryptophan (trp) promoter
5 system; and hybrid promoters such as the tac promoter. Other known bacterial promoters are also suitable. Their nucleotide sequences have been published, thereby enabling one skilled in the art to ligate them to the desired DNA sequence(s), using linkers or adaptors as needed to supply any required restriction sites.

Suitable promoting sequences for use with yeast hosts are also well known in
10 the art. Yeast enhancers are advantageously used with yeast promoters. Suitable promoters for use with mammalian host cells are well known and include those obtained from the genomes of viruses such as polyoma virus, fowlpox virus, adenovirus (such as Adenovirus 2), bovine papilloma virus, avian sarcoma virus, cytomegalovirus, a retrovirus, hepatitis-B virus and most preferably Simian Virus 40
15 (SV40). Other suitable mammalian promoters include heterologous mammalian promoters, e.g., heat-shock promoters and the actin promoter. A promoter for possible use in the production of GDNFR proteins in CHO cells is SRa (see Takebe et al., Mol. Cell. Biol., 8(1): 466-472, 1988). A suitable expression vector is pDSRa2. The pDSRa2 plasmid constructs containing the appropriate GDNFR cDNA may be
20 prepared substantially in accordance with the process described in the co-owned and copending U. S. Patent Application Serial Number 501,904 filed March 29, 1990 (also see, European Patent Application No. 90305433, Publication No. EP 398 753, filed May 18, 1990 and WO 90/14363 (1990), the disclosures of which are hereby incorporated by reference.

25 Additional promoters which may be of interest in controlling GDNFR expression include, but are not limited to: the SV40 early promoter region (Bernoist and Chambon, Nature, 290:304-310, 1981); the CMV promoter; the promoter contained in the 3' long terminal repeat of Rous sarcoma virus (Yamamoto, et al., Cell, 22:787-797, 1980); the herpes thymidine kinase promoter (Wagner et al., Proc.
30 Natl. Acad. Sci. U.S.A., 78:144-1445, 1981); the regulatory sequences of the metallothionine gene (Brinster et al., Nature, 296:39-42, 1982); prokaryotic expression vectors such as the beta -lactamase promoter (Villa-Kamaroff, et al., Proc. Natl. Acad. Sci. U.S.A., 75:3727-3731, 1978); or the tac promoter (DeBoer, et al., Proc. Natl. Acad. Sci. U.S.A., 80:21-25, 1983). Also of interest are the following
35 animal transcriptional control regions, which exhibit tissue specificity and have been utilized in transgenic animals: the elastase I gene control region which is active in pancreatic acinar cells (Swift et al., Cell, 38:639-646, 1984; Ornitz et al., Cold Spring

Harbor Symp. Quant. Biol. 50:399-409, 1986; MacDonald, Hepatology, 7:425-515, 1987); the insulin gene control region which is active in pancreatic beta cells (Hanahan, Nature, 315:115-122, 1985); the immunoglobulin gene control region which is active in lymphoid cells (Grosschedl et al., Cell, 38:647-658, 1984; Adames et al., Nature, 318:533-538, 1985; Alexander et al., Mol. Cell. Biol., 7:1436-1444, 1987); the mouse mammary tumor virus control region which is active in testicular, breast, lymphoid and mast cells (Leder et al., Cell, 45:485-495, 1986), albumin gene control region which is active in liver (Pinkert et al., Genes and Devel., 1:268-276, 1987); the alpha-fetoprotein gene control region which is active in liver (Krumlauf et al., Mol. Cell. Biol., 5:1639-1648, 1985; Hammer et al., Science, 235:53-58, 1987); the alpha 1-antitrypsin gene control region which is active in the liver (Kelsey et al., Genes and Devel., 1:161-171, 1987); the beta-globin gene control region which is active in myeloid cells (Mogram et al., Nature, 315:338-340, 1985; Kollias et al., Cell, 46:89-94, 1986); the myelin basic protein gene control region which is active in oligodendrocyte cells in the brain (Readhead et al., Cell, 48:703-712, 1987); the myosin light chain-2 gene control region which is active in skeletal muscle (Sani, Nature, 314:283-286, 1985); and the gonadotropic releasing hormone gene control region which is active in the hypothalamus (Mason et al., Science, 234:1372-1378, 1986).

20

Enhancer Element

An enhancer sequence may be inserted into the vector to increase the transcription of a DNA sequence encoding a GDNFR protein of the present invention by higher eukaryotes. Enhancers are cis-acting elements of DNA, usually about 10-300 bp in length, that act on the promoter to increase its transcription. Enhancers are relatively orientation and position independent. They have been found 5' and 3' to the transcription unit. Several enhancer sequences available from mammalian genes are known (e.g., globin, elastase, albumin, alpha-feto-protein and insulin). Typically, however, an enhancer from a virus will be used. The SV40 enhancer, the cytomegalovirus early promoter enhancer, the polyoma enhancer, and adenovirus enhancers are exemplary enhancing elements for the activation of eukaryotic promoters. While an enhancer may be spliced into the vector at a position 5' or 3' to GDNFR DNA, it is typically located at a site 5' from the promoter.

Transcription Termination

Expression vectors used in eukaryotic host cells (yeast, fungi, insect, plant, animal, human, or nucleated cells from other multicellular organisms) will also contain

sequences necessary for terminating transcription and stabilizing the mRNA. Such sequences are commonly available from the 5' and occasionally 3' untranslated regions of eukaryotic DNAs or cDNAs. These regions contain nucleotide segments transcribed as polyadenylated fragments in the untranslated portion of the mRNA encoding GDNFR.

The construction of suitable vectors containing one or more of the above-listed components together with the desired GDNFR-encoding sequence is accomplished by standard ligation techniques. Isolated plasmids or DNA fragments are cleaved, tailored, and religated in the desired order to generate the plasmids required. To confirm that the correct sequences have been constructed, the ligation mixtures may be used to transform *E. coli*, and successful transformants may be selected by known techniques, such as ampicillin or tetracycline resistance as described above. Plasmids from the transformants may then be prepared, analyzed by restriction endonuclease digestion, and/or sequenced to confirm the presence of the desired construct.

Vectors that provide for the transient expression of DNA encoding GDNFR in mammalian cells may also be used. In general, transient expression involves the use of an expression vector that is able to replicate efficiently in a host cell, such that the host cell accumulates many copies of the expression vector and, in turn, synthesizes high levels of the desired protein encoded by the expression vector. Transient expression systems, comprising a suitable expression vector and a host cell, allow for the convenient positive identification of proteins encoded by cloned DNAs, as well as for the rapid screening of such proteins for desired biological or physiological properties. Thus, transient expression systems are particularly useful in identifying variants of the protein.

Selection and Transformation of Host Cells

Host cells (e.g., bacterial, mammalian, insect, yeast, or plant cells) transformed with nucleic acid sequences for use in expressing a recombinant GDNFR protein are also provided by the present invention. The transformed host cell is cultured under appropriate conditions permitting the expression of the nucleic acid sequence. The selection of suitable host cells and methods for transformation, culture, amplification, screening and product production and purification are well known in the art. See for example, Gething and Sambrook, *Nature*, 293: 620-625 (1981), or alternatively, Kaufman et al., *Mol. Cell. Biol.*, 5 (7): 1750-1759 (1985) or Howley et al., U.S. Pat. No. 4,419,446. Additional exemplary materials and methods are discussed herein. The transformed host cell is cultured in a suitable medium, and the

expressed GDNFR protein is then optionally recovered, isolated and purified from the culture medium (or from the cell, if expressed intracellularly) by an appropriate means known to those skilled in the art.

5 Different host cells have characteristic and specific mechanisms for the translational and post-translational processing and modification (e.g., glycosylation, cleavage) of proteins. Appropriate cell lines or host systems can be chosen to ensure the desired modification and processing of the foreign protein expressed. For example, expression in a bacterial system can be used to produce an unglycosylated core protein product. Expression in yeast may be used to produce a glycosylated
10 product. Expression in mammalian cells can be used to ensure "native" glycosylation of the heterologous GDNFR protein. Furthermore, different vector/host expression systems may effect processing reactions such as proteolytic cleavages to different extents.

Suitable host cells for cloning or expressing the vectors disclosed herein are
15 prokaryote, yeast, or higher eukaryote cells. Eukaryotic microbes such as filamentous fungi or yeast may be suitable hosts for the expression of GDNFR proteins. *Saccharomyces cerevisiae*, or common baker's yeast, is the most commonly used among lower eukaryotic host microorganisms, but a number of other genera, species, and strains are well known and commonly available.

20 Host cells to be used for the expression of glycosylated GDNFR protein are also derived from multicellular organisms. Such host cells are capable of complex processing and glycosylation activities. In principle, any higher eukaryotic cell culture might be used, whether such culture involves vertebrate or invertebrate cells, including plant and insect cells. The propagation of vertebrate cells in culture (tissue culture) is a well known procedure. Examples of useful mammalian host cell lines include, but are
25 not limited to, monkey kidney CV1 line transformed by SV40 (COS7), human embryonic kidney line (293 or 293 cells subcloned for growth in suspension culture), baby hamster kidney cells, and Chinese hamster ovary cells. Other suitable mammalian cell lines include but are not limited to, HeLa, mouse L-929 cells,
30 3T3 lines derived from Swiss, Balb-c or NIH mice, BHK or HaK hamster cell lines.

Suitable host cells also include prokaryotic cells. Prokaryotic host cells include, but are not limited to, bacterial cells, such as Gram-negative or Gram-positive organisms, for example, *E. coli*, Bacilli such as *B. subtilis*, *Pseudomonas* species such as *P. aeruginosa*, *Salmonella typhimurium*, or *Serratia marcescans*. For
35 example, the various strains of *E. coli* (e.g., HB101, DH5a, DH10, and MC1061) are well-known as host cells in the field of biotechnology. Various strains of *Streptomyces* spp. and the like may also be employed. Presently preferred host cells

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Suitable host cells for cloning or expressing the vectors disclosed herein are prokaryote, yeast, or higher eukaryote cells. Eukaryotic microbes such as filamentous fungi or yeast may be suitable hosts for the expression of GDNFR proteins. *Saccharomyces cerevisiae*, or common baker's yeast, is the most commonly used among lower eukaryotic host microorganisms, but a number of other genera, species, and strains are well known and commonly available.

Host cells to be used for the expression of glycosylated GDNFR protein are also derived from multicellular organisms. Such host cells are capable of complex processing and glycosylation activities. In principle, any higher eukaryotic cell culture might be used, whether such culture involves vertebrate or invertebrate cells, including plant and insect cells. The propagation of vertebrate cells in culture (tissue culture) is a well known procedure. Examples of useful mammalian host cell lines include, but are not limited to, monkey kidney CV1 line transformed by SV40 (COS7), human embryonic kidney line (293 or 293 cells subcloned for growth in suspension culture), baby hamster kidney cells, and Chinese hamster ovary cells. Other suitable mammalian cell lines include but are not limited to, HeLa, mouse L-929 cells, 3T3 lines derived from Swiss, Balb-c or NIH mice, BHK or HaK hamster cell lines.

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for producing GDNFR proteins are bacterial cells (e.g., *Escherichia coli*) and mammalian cells (such as Chinese hamster ovary cells, COS cells, etc.)

The host cells are transfected and preferably transformed with the above-described expression or cloning vectors and cultured in a conventional nutrient medium. The medium may be modified as appropriate for inducing promoters, selecting transformants, or amplifying the genes encoding the desired sequences. Transfection and transformation are performed using standard techniques which are well known to those skilled in the art and which are selected as appropriate to the host cell involved. For example, for mammalian cells without cell walls, the calcium phosphate precipitation method may be used. Electroporation, micro injection and other known techniques may also be used.

Culturing the Host Cells

Transformed cells used to produce GDNFR proteins of the present invention are cultured in suitable media. The media may be supplemented as necessary with hormones and/or other growth factors (such as insulin, transferrin, or epidermal growth factor), salts (such as sodium chloride, calcium, magnesium, and phosphate), buffers (such as HEPES), nucleosides (such as adenosine and thymidine), antibiotics (such as gentamicin), trace elements (defined as inorganic compounds usually present at final concentrations in the micromolar range), and glucose or other energy source. Other supplements may also be included, at appropriate concentrations, as will be appreciated by those skilled in the art. Suitable culture conditions, such as temperature, pH, and the like, are also well known to those skilled in the art for use with the selected host cells.

Once the GDNFR protein is produced, it may be isolated and purified by standard methods including chromatography (e.g., ion exchange, affinity, and sizing column chromatography), centrifugation, differential solubility, or by any other standard technique for the purification of proteins. In particular, GDNFR protein may be isolated by binding to an affinity column comprising GDNF or anti-GDNFR antibody bound to a stationary support.

Homologous Recombination

It is further envisioned that GDNFR proteins may be produced by homologous recombination, or with recombinant production methods utilizing control elements introduced into cells already containing DNA encoding GDNFR. For example, homologous recombination methods may be used to modify a cell that contains a normally transcriptionally silent GDNFR gene or under expressed gene and thereby

produce a cell which expresses GDNFR. Homologous recombination is a technique originally developed for targeting genes to induce or correct mutations in transcriptionally active genes (Kucherlapati, Prog. in Nucl. Acid Res. and Mol. Biol., 36:301, 1989). The basic technique was developed as a method for introducing
5 specific mutations into specific regions of the mammalian genome (Thomas et al., Cell, 44:419-428, 1986; Thomas and Capecchi, Cell, 51:503-512, 1987; Doetschman et al., Proc. Natl. Acad. Sci., 85:8583-8587, 1988) or to correct specific mutations within defective genes (Doetschman et al., Nature, 330:576-578, 1987). Exemplary homologous recombination techniques are described in U.S. 5,272,071
10 (EP 91 90 3051, EP Publication No. 505 500; PCT/US90/07642, International Publication No. WO 91/09955) the disclosure of which is hereby incorporated by reference.

Through homologous recombination, the DNA sequence to be inserted into the genome can be directed to a specific region of the gene of interest by attaching it to
15 targeting DNA. The targeting DNA is DNA that is complementary (homologous) to a region of the genomic DNA. Small pieces of targeting DNA that are complementary to a specific region of the genome are put in contact with the parental strand during the DNA replication process. It is a general property of DNA that has been inserted into a cell to hybridize, and therefore, recombine with other pieces of endogenous DNA
20 through shared homologous regions. If this complementary strand is attached to an oligonucleotide that contains a mutation or a different sequence of DNA, it too is incorporated into the newly synthesized strand as a result of the recombination. As a result of the proofreading function, it is possible for the new sequence of DNA to serve as the template. Thus, the transferred DNA is incorporated into the genome.

25 If the sequence of a particular gene is known, such as the nucleic acid sequence, the pre-pro sequence or expression control sequence of GDNFR presented herein, a piece of DNA that is complementary to a selected region of the gene can be synthesized or otherwise obtained, such as by appropriate restriction of the native DNA at specific recognition sites bounding the region of interest. This piece serves as
30 a targeting sequence upon insertion into the cell and will hybridize to its homologous region within the genome. If this hybridization occurs during DNA replication, this piece of DNA, and any additional sequence attached thereto, will act as an Okazaki fragment and will be backstitched into the newly synthesized daughter strand of DNA.

Attached to these pieces of targeting DNA are regions of DNA which may
35 interact with the expression of a GDNFR protein. For example, a promoter/enhancer element, a suppresser, or an exogenous transcription modulatory element is inserted in the genome of the intended host cell in proximity and orientation sufficient to influence

the transcription of DNA encoding the desired GDNFR protein. The control element does not encode GDNFR, but instead controls a portion of the DNA present in the host cell genome. Thus, the expression of GDNFR proteins may be achieved not by transfection of DNA that encodes the GDNFR gene itself, but rather by the use of targeting DNA (containing regions of homology with the endogenous gene of interest) coupled with DNA regulatory segments that provide the endogenous gene sequence with recognizable signals for transcription of a GDNFR protein.

A. GDNFR variants

As discussed above, the terms "GDNFR analogs" as used herein include polypeptides in which amino acids have been deleted from ("deletion variants"), inserted into ("addition variants"), or substituted for ("substitution variants") residues within the amino acid sequence of naturally-occurring GDNFR polypeptides including those depicted in Figures 2 and 4 (SEQ. ID. NOs.:2 and 4). Such variants are prepared by introducing appropriate nucleotide changes into the DNA encoding the polypeptide or by in vitro chemical synthesis of the desired polypeptide. It will be appreciated by those skilled in the art that many combinations of deletions, insertions, and substitutions can be made to an amino acid sequence such as mature human GDNFR provided that the final molecule possesses GDNFR activity.

Based upon the present description of GDNFR amino acid sequences, one can readily design and manufacture a variety of nucleic acid sequences suitable for use in the recombinant (e.g., microbial) expression of polypeptides having primary conformations which differ from those depicted in the Figures in terms of the identity or location of one or more residues. Mutagenesis techniques for the replacement, insertion or deletion of one or more selected amino acid residues encoded by the nucleic acid sequences depicted in Figures 2 and 4 are well known to one skilled in the art (e.g., U.S. Pat. No. 4,518,584, the disclosure of which is hereby incorporated by reference.) There are two principal variables in the construction of substitution variants: the location of the mutation site and the nature of the mutation. In designing GDNFR substitution variants, the selection of the mutation site and nature of the mutation will depend on the GDNFR characteristic(s) to be modified. The sites for mutation can be modified individually or in series, e.g., by (1) substituting first with conservative amino acid modifications and then with more radical selections depending upon the results achieved, (2) deleting the target amino acid residue, or (3) inserting amino acid residues adjacent to the located site. Conservative changes in from 1 to 30 contiguous amino acids are preferred. N-terminal and C-terminal deletion GDNFR protein variants may also be generated by proteolytic enzymes.

For GDNFR deletion variants, deletions generally range from about 1 to 30 contiguous residues, more usually from about 1 to 10 contiguous residues, and typically from about 1 to 5 contiguous residues. N-terminal, C-terminal and internal intrasequence deletions are contemplated. Deletions may be introduced into regions of the molecule which have low homology with non-human GDNFR to modify the activity of GDNFR. Deletions in areas of substantial homology with non-human GDNFR sequences will be more likely to significantly modify GDNFR biological activity. The number of consecutive deletions typically will be selected so as to preserve the tertiary structure of the GDNFR protein product in the affected domain, e.g., cysteine crosslinking. Non-limiting examples of deletion variants include truncated GDNFR protein products lacking N-terminal or C-terminal amino acid residues. For example, one may prepare a soluble receptor by elimination of the peptide region involved in a glycosyl-phosphatidylinositol (GPI) anchorage of GDNFR receptor to the cytoplasmic membrane.

For GDNFR addition variants, amino acid sequence additions typically include N-and/or C-terminal fusions or terminal additions ranging in length from one residue to polypeptides containing a hundred or more residues, as well as internal or medial additions of single or multiple amino acid residues. Polypeptides of the invention may also include an initial methionine amino acid residue (at position -1 with respect to the first amino acid residue of the desired polypeptide). Internal additions may range generally from about 1 to 10 contiguous residues, more typically from about 1 to 5 residues, and usually from about 1 to 3 amino acid residues. Examples of N-terminal addition variants include GDNFR with the inclusion of a heterologous N-terminal signal sequence to the N-terminus of GDNFR to facilitate the secretion of mature GDNFR from recombinant host cells and thereby facilitate harvesting or bioavailability. Such signal sequences generally will be obtained from, and thus be homologous to, the intended host cell species. Additions may also include amino acid sequences derived from the sequence of other neurotrophic factors. For example, it is contemplated that a fusion protein of GDNF and GDNFR may be produced, with or without a linking sequence, thereby forming a single molecule therapeutic entity.

GDNFR substitution variants have one or more amino acid residues of the GDNFR amino acid sequence removed and a different residue(s) inserted in its place. Such substitution variants include allelic variants, which are characterized by naturally-occurring nucleotide sequence changes in the species population that may or may not result in an amino acid change. As with the other variant forms, substitution variants may involve the replacement of single or contiguous amino acid residues at one or more different locations.

Specific mutations of the GDNFR amino acid sequence may involve modifications to a glycosylation site (e.g., serine, threonine, or asparagine). The absence of glycosylation or only partial glycosylation results from amino acid substitution or deletion at any asparagine-linked glycosylation recognition site or at any site of the molecule that is modified by addition of an O-linked carbohydrate. An asparagine-linked glycosylation recognition site comprises a tripeptide sequence which is specifically recognized by appropriate cellular glycosylation enzymes. These tripeptide sequences are either Asn-Xaa-Thr or Asn-Xaa-Ser, where Xaa can be any amino acid other than Pro. A variety of amino acid substitutions or deletions at one or both of the first or third amino acid positions of a glycosylation recognition site (and/or amino acid deletion at the second position) result in non-glycosylation at the modified tripeptide sequence. Thus, the expression of appropriate altered nucleotide sequences produces variants which are not glycosylated at that site. Alternatively, the GDNFR amino acid sequence may be modified to add glycosylation sites.

One method for identifying GDNFR amino acid residues or regions for mutagenesis is called "alanine scanning mutagenesis" as described by Cunningham and Wells (Science, 244: 1081-1085, 1989). In this method, an amino acid residue or group of target residues are identified (e.g., charged residues such as Arg, Asp, His, Lys, and Glu) and replaced by a neutral or negatively charged amino acid (most preferably alanine or polyalanine) to affect the interaction of the amino acids with the surrounding aqueous environment in or outside the cell. Those domains demonstrating functional sensitivity to the substitutions may then be refined by introducing additional or alternate residues at the sites of substitution. Thus, the target site for introducing an amino acid sequence variation is determined, alanine scanning or random mutagenesis is conducted on the corresponding target codon or region of the DNA sequence, and the expressed GDNFR variants are screened for the optimal combination of desired activity and degree of activity.

The sites of greatest interest for substitutional mutagenesis include sites where the amino acids found in GDNFR proteins from various species are substantially different in terms of side-chain bulk, charge, and/or hydrophobicity. Other sites of interest are those in which particular residues of GDNFR-like proteins, obtained from various species, are identical. Such positions are generally important for the biological activity of a protein. Initially, these sites are substituted in a relatively conservative manner. Such conservative substitutions are shown in Table 2 under the heading of preferred substitutions. If such substitutions result in a change in biological activity, then more substantial changes (exemplary substitutions) may be introduced, and/or other additions or deletions may be made, and the resulting products are screened for

activity.

TABLE 2
Amino Acid Substitutions

5

<u>Original Residue</u>	<u>Preferred Substitutions</u>	<u>Exemplary Substitutions</u>
Ala (A)	Val	Val; Leu; Ile
Arg (R)	Lys	Lys; Gln; Asn
Asn (N)	Gln	Gln; His; Lys; Arg
Asp (D)	Glu	Glu
Cys (C)	Ser	Ser
Gln (Q)	Asn	Asn
Glu (E)	Asp	Asp
Gly (G)	Pro	Pro
His (H)	Arg	Asn; Gln; Lys; Arg
Ile (I)	Leu	Leu; Val; Met; Ala; Phe; norleucine
Leu (L)	Ile	norleucine; Ile; Val; Met; Ala; Phe
Lys (K)	Arg	Arg; Gln; Asn
Met (M)	Leu	Leu; Phe; Ile
Phe (F)	Leu	Leu; Val; Ile; Ala
Pro (P)	Gly	Gly
Ser (S)	Thr	Thr
Thr (T)	Ser	Ser
Trp (W)	Tyr	Tyr
Tyr (Y)	Phe	Trp; Phe; Thr; Ser
Val (V)	Leu	Ile; Leu; Met; Phe; Ala; norleucine

Conservative modifications to the amino acid sequence (and the corresponding modifications to the encoding nucleic acid sequences) are expected to produce GDNFR protein products having functional and chemical characteristics similar to those of naturally occurring GDNFR. In contrast, substantial modifications in the functional and/or chemical characteristics of GDNFR protein products may be accomplished by selecting substitutions that differ significantly in their effect on maintaining (a) the

10

structure of the polypeptide backbone in the area of the substitution, for example, as a sheet or helical conformation, (b) the charge or hydrophobicity of the molecule at the target site, or (c) the bulk of the side chain. Naturally occurring residues may be divided into groups based on common side chain properties:

- 5 1) hydrophobic: norleucine, Met, Ala, Val, Leu, Ile;
- 2) neutral hydrophilic: Cys, Ser, Thr;
- 3) acidic: Asp, Glu;
- 4) basic: Asn, Gln, His, Lys, Arg;
- 5) residues that influence chain orientation: Gly, Pro; and
- 10 6) aromatic: Trp, Tyr, Phe.

Non-conservative substitutions may involve the exchange of a member of one of these classes for a member from another class. Such substituted residues may be introduced into regions of the human GDNFR protein that are homologous with non-human GDNFR proteins, or into the non-homologous regions of the molecule.

- 15 Thus, GDNFR proteins, analogs, or derivatives thereof include, but are not limited to, those biologically active molecules containing, as a primary amino acid sequence, all or part of the amino acid sequences as depicted in Figures 2 and 4 (SEQ ID NOs. 2 and 4). The proteins will include altered sequences in which biologically equivalent amino acid residues are substituted for residues within the sequence
- 20 resulting in a silent change. For example, one or more amino acid residues within the sequence can be substituted by another amino acid of a similar polarity which acts as a functional equivalent, resulting in a silent alteration. Substitutes for an amino acid within the sequence may be selected from other members of the class to which the amino acid belongs. For example, the nonpolar (hydrophobic) amino acids include
- 25 alanine, leucine, isoleucine, valine, proline, phenylalanine, tryptophan and methionine. The polar neutral amino acids include glycine, serine, threonine, cysteine, tyrosine, asparagine, and glutamine. The positively charged (basic) amino acids include arginine, lysine and histidine. The negatively charged (acidic) amino acids include aspartic acid and glutamic acid. It is also contemplated that the GDNFR
- 30 proteins, analogs, or fragments or derivatives thereof may be differentially modified during or after translation, e.g., by phosphorylation, glycosylation, crosslinking, acylation, proteolytic cleavage, linkage to an antibody molecule, membrane molecule or other ligand.

35 B. GDNFR Derivatives

Chemically modified derivatives of GDNFR or GDNFR analogs may be prepared by one of skill in the art based upon the present disclosure. The chemical

moieties most suitable for derivatization include water soluble polymers. A water soluble polymer is desirable because the protein to which it is attached does not precipitate in an aqueous environment, such as a physiological environment. Preferably, the polymer will be pharmaceutically acceptable for the preparation of a therapeutic product or composition. One skilled in the art will be able to select the desired polymer based on such considerations as whether the polymer/protein conjugate will be used therapeutically, and if so, the desired dosage, circulation time, resistance to proteolysis, and other considerations. The effectiveness of the derivatization may be ascertained by administering the derivative, in the desired form (e.g., by osmotic pump, or, more preferably, by injection or infusion, or, further formulated for oral, pulmonary or other delivery routes), and determining its effectiveness.

Suitable water soluble polymers include, but are not limited to, polyethylene glycol, copolymers of ethylene glycol/propylene glycol, carboxymethylcellulose, dextran, polyvinyl alcohol, polyvinyl pyrrolidone, poly-1, 3-dioxolane, poly-1,3,6-trioxane, ethylene/maleic anhydride copolymer, polyaminoacids (either homopolymers or random copolymers), and dextran or poly(n-vinyl pyrrolidone)polyethylene glycol, propylene glycol homopolymers, polypropylene oxide/ethylene oxide copolymers, polyoxyethylated polyols (e.g., glycerol), polyvinyl alcohol, and mixtures thereof. Polyethylene glycol propionaldehyde may have advantages in manufacturing due to its stability in water.

The polymer may be of any molecular weight, and may be branched or unbranched. For polyethylene glycol, the preferred molecular weight is between about 2 kDa and about 100 kDa for ease in handling and manufacturing (the term "about" indicating that in preparations of polyethylene glycol, some molecules will weigh more, some less, than the stated molecular weight). Other sizes may be used, depending on the desired therapeutic profile (e.g., the duration of sustained release desired; the effects, if any, on biological activity; the ease in handling; the degree or lack of antigenicity and other known effects of polyethylene glycol on a therapeutic protein or variant).

The number of polymer molecules so attached may vary, and one skilled in the art will be able to ascertain the effect on function. One may mono-derivatize, or may provide for a di-, tri-, tetra- or some combination of derivatization, with the same or different chemical moieties (e.g., polymers, such as different weights of polyethylene glycols). The proportion of polymer molecules to protein (or peptide) molecules will vary, as will their concentrations in the reaction mixture. In general, the optimum ratio (in terms of efficiency of reaction in that there is no excess unreacted protein or

polymer) will be determined by factors such as the desired degree of derivatization (e.g., mono, di-, tri-, etc.), the molecular weight of the polymer selected, whether the polymer is branched or unbranched, and the reaction conditions.

The polyethylene glycol molecules (or other chemical moieties) should be
5 attached to the protein with consideration of effects on functional or antigenic domains of the protein. There are a number of attachment methods available to those skilled in the art. See for example, EP 0 401 384, the disclosure of which is hereby incorporated by reference (coupling PEG to G-CSF), see also Malik et al., Exp. Hematol., 20: 1028-1035, 1992 (reporting pegylation of GM-CSF using tresyl
10 chloride). For example, polyethylene glycol may be covalently bound through amino acid residues via a reactive group, such as, a free amino or carboxyl group. Reactive groups are those to which an activated polyethylene glycol molecule may be bound. The amino acid residues having a free amino group may include lysine residues and the N-terminal amino acid residue. Those having a free carboxyl group may include
15 aspartic acid residues, glutamic acid residues, and the C-terminal amino acid residue. Sulfhydryl groups may also be used as a reactive group for attaching the polyethylene glycol molecule(s). For therapeutic purposes, attachment at an amino group, such as attachment at the N-terminus or lysine group is preferred. Attachment at residues important for receptor binding should be avoided if receptor binding is desired.

20 One may specifically desire an N-terminal chemically modified protein. Using polyethylene glycol as an illustration of the present compositions, one may select from a variety of polyethylene glycol molecules (by molecular weight, branching, etc.), the proportion of polyethylene glycol molecules to protein (or peptide) molecules in the reaction mix, the type of pegylation reaction to be performed, and the method of
25 obtaining the selected N-terminally pegylated protein. The method of obtaining the N-terminally pegylated preparation (i.e., separating this moiety from other monopegylated moieties if necessary) may be by purification of the N-terminally pegylated material from a population of pegylated protein molecules. Selective N-terminal chemical modification may be accomplished by reductive alkylation which
30 exploits differential reactivity of different types of primary amino groups (lysine versus the N-terminal) available for derivatization in a particular protein. Under the appropriate reaction conditions, substantially selective derivatization of the protein at the N-terminus with a carbonyl group containing polymer is achieved. For example, one may selectively N-terminally pegylate the protein by performing the reaction at a
35 pH which allows one to take advantage of the pKa differences between the ϵ -amino group of the lysine residues and that of the α -amino group of the N-terminal residue of the protein. By such selective derivatization, attachment of a water soluble polymer to

a protein is controlled: the conjugation with the polymer takes place predominantly at the N-terminus of the protein and no significant modification of other reactive groups, such as the lysine side chain amino groups, occurs. Using reductive alkylation, the water soluble polymer may be of the type described above, and should have a single reactive aldehyde for coupling to the protein. Polyethylene glycol propionaldehyde, containing a single reactive aldehyde, may be used.

The present invention contemplates use of derivatives which are prokaryote-expressed GDNFR, or variants thereof, linked to at least one polyethylene glycol molecule, as well as use of GDNFR, or variants thereof, attached to one or more polyethylene glycol molecules via an acyl or alkyl linkage.

Pegylation may be carried out by any of the pegylation reactions known in the art. See, for example: Focus on Growth Factors, 3 (2): 4-10, 1992; EP 0 154 316, the disclosure of which is hereby incorporated by reference; EP 0 401 384; and the other publications cited herein that relate to pegylation. The pegylation may be carried out via an acylation reaction or an alkylation reaction with a reactive polyethylene glycol molecule (or an analogous reactive water-soluble polymer).

Pegylation by acylation generally involves reacting an active ester derivative of polyethylene glycol (PEG) with the GDNFR protein or variant. Any known or subsequently discovered reactive PEG molecule may be used to carry out the pegylation of GDNFR protein or variant. A preferred activated PEG ester is PEG esterified to N-hydroxysuccinimide (NHS). As used herein, "acylation" is contemplated to include without limitation the following types of linkages between the therapeutic protein and a water soluble polymer such as PEG: amide, carbamate, urethane, and the like. See Bioconjugate Chem., 5: 133-140, 1994. Reaction conditions may be selected from any of those known in the pegylation art or those subsequently developed, but should avoid conditions such as temperature, solvent, and pH that would inactivate the GDNFR or variant to be modified.

Pegylation by acylation will generally result in a poly-pegylated GDNFR protein or variant. Preferably, the connecting linkage will be an amide. Also preferably, the resulting product will be substantially only (e.g., > 95%) mono, di- or tri-pegylated. However, some species with higher degrees of pegylation may be formed in amounts depending on the specific reaction conditions used. If desired, more purified pegylated species may be separated from the mixture, particularly unreacted species, by standard purification techniques, including, among others, dialysis, salting-out, ultrafiltration, ion-exchange chromatography, gel filtration chromatography and electrophoresis.

Pegylation by alkylation generally involves reacting a terminal aldehyde

derivative of PEG with the GDNFR protein or variant in the presence of a reducing agent. Pegylation by alkylation can also result in poly-pegylated GDNFR protein or variant. In addition, one can manipulate the reaction conditions to favor pegylation substantially only at the α -amino group of the N-terminus of the GDNFR protein or variant (i.e., a mono-pegylated protein). In either case of monopegylation or polypegylation, the PEG groups are preferably attached to the protein via a $-\text{CH}_2\text{-NH-}$ group. With particular reference to the $-\text{CH}_2\text{-}$ group, this type of linkage is referred to herein as an "alkyl" linkage.

Derivatization via reductive alkylation to produce a monopegylated product exploits differential reactivity of different types of primary amino groups (lysine versus the N-terminal) available for derivatization. The reaction is performed at a pH which allows one to take advantage of the pKa differences between the ϵ -amino groups of the lysine residues and that of the α -amino group of the N-terminal residue of the protein. By such selective derivatization, attachment of a water soluble polymer that contains a reactive group such as an aldehyde, to a protein is controlled: the conjugation with the polymer takes place predominantly at the N-terminus of the protein and no significant modification of other reactive groups, such as the lysine side chain amino groups, occurs. In one important aspect, the present invention contemplates use of a substantially homogeneous preparation of monopolymer/GDNFR protein (or variant) conjugate molecules (meaning GDNF protein or variant to which a polymer molecule has been attached substantially only (i.e., > 95%) in a single location). More specifically, if polyethylene glycol is used, the present invention also encompasses use of pegylated GDNFR protein or variant lacking possibly antigenic linking groups, and having the polyethylene glycol molecule directly coupled to the GDNFR protein or variant.

Thus, GDNFR protein products according to the present invention include pegylated GDNFR protein or variants, wherein the PEG group(s) is (are) attached via acyl or alkyl groups. As discussed above, such products may be mono-pegylated or poly-pegylated (e.g., containing 2-6, and preferably 2-5, PEG groups). The PEG groups are generally attached to the protein at the α - or ϵ -amino groups of amino acids, but it is also contemplated that the PEG groups could be attached to any amino group attached to the protein, which is sufficiently reactive to become attached to a PEG group under suitable reaction conditions.

The polymer molecules used in both the acylation and alkylation approaches may be selected from among water soluble polymers as described above. The polymer selected should be modified to have a single reactive group, such as an active ester for acylation or an aldehyde for alkylation, preferably, so that the degree of polymerization

may be controlled as provided for in the present methods. An exemplary reactive PEG aldehyde is polyethylene glycol propionaldehyde, which is water stable, or mono C1-C10 alkoxy or aryloxy derivatives thereof (see, U.S. Patent 5,252,714). The polymer may be branched or unbranched. For the acylation reactions, the polymer(s) selected should have a single reactive ester group. For the present reductive alkylation, the polymer(s) selected should have a single reactive aldehyde group. Generally, the water soluble polymer will not be selected from naturally-occurring glycosyl residues since these are usually made more conveniently by mammalian recombinant expression systems. The polymer may be of any molecular weight, and may be branched or unbranched.

An exemplary water-soluble polymer for use herein is polyethylene glycol. As used herein, polyethylene glycol is meant to encompass any of the forms of PEG that have been used to derivatize other proteins, such as mono-(C1-C10) alkoxy- or aryloxy-polyethylene glycol.

In general, chemical derivatization may be performed under any suitable condition used to react a biologically active substance with an activated polymer molecule. Methods for preparing a pegylated GDNFR protein product will generally comprise the steps of (a) reacting a GDNFR protein product with polyethylene glycol (such as a reactive ester or aldehyde derivative of PEG) under conditions whereby the protein becomes attached to one or more PEG groups, and (b) obtaining the reaction product(s). In general, the optimal reaction conditions for the acylation reactions will be determined case-by-case based on known parameters and the desired result. For example, the larger the ratio of PEG:protein, the greater the percentage of poly-pegylated product.

Reductive alkylation to produce a substantially homogeneous population of mono-polymer/GDNFR protein product will generally comprise the steps of: (a) reacting a GDNFR protein or variant with a reactive PEG molecule under reductive alkylation conditions, at a pH suitable to permit selective modification of the α -amino group at the amino terminus of said GDNFR protein or variant; and (b) obtaining the reaction product(s).

For a substantially homogeneous population of mono-polymer/GDNFR protein product, the reductive alkylation reaction conditions are those which permit the selective attachment of the water soluble polymer moiety to the N-terminus of GDNFR protein or variant. Such reaction conditions generally provide for pKa differences between the lysine amino groups and the α -amino group at the N-terminus (the pKa being the pH at which 50% of the amino groups are protonated and 50% are not). The pH also affects the ratio of polymer to protein to be used. In general, if the pH is

lower, a larger excess of polymer to protein will be desired (i.e., the less reactive the N-terminal α -amino group, the more polymer needed to achieve optimal conditions). If the pH is higher, the polymer:protein ratio need not be as large (i.e., more reactive groups are available, so fewer polymer molecules are needed). For purposes of the present invention, the pH will generally fall within the range of 3-9, preferably 3-6.

Another important consideration is the molecular weight of the polymer. In general, the higher the molecular weight of the polymer, the fewer polymer molecules may be attached to the protein. Similarly, branching of the polymer should be taken into account when optimizing these parameters. Generally, the higher the molecular weight (or the more branches) the higher the polymer:protein ratio. In general, for the pegylation reactions contemplated herein, the preferred average molecular weight is about 2 kDa to about 100 kDa. The preferred average molecular weight is about 5 kDa to about 50 kDa, particularly preferably about 12 kDa to about 25 kDa. The ratio of water-soluble polymer to GDNF protein or variant will generally range from 1:1 to 100:1, preferably (for polypegylation) 1:1 to 20:1 and (for monopegylation) 1:1 to 5:1.

Using the conditions indicated above, reductive alkylation will provide for selective attachment of the polymer to any GDNFR protein or variant having an α -amino group at the amino terminus, and provide for a substantially homogenous preparation of monopolymer/GDNFR protein (or variant) conjugate. The term "monopolymer/GDNFR protein (or variant) conjugate" is used here to mean a composition comprised of a single polymer molecule attached to a molecule of GDNFR protein or GDNFR variant protein. The monopolymer/GDNFR protein (or variant) conjugate typically will have a polymer molecule located at the N-terminus, but not on lysine amino side groups. The preparation will generally be greater than 90% monopolymer/GDNFR protein (or variant) conjugate, and more usually greater than 95% monopolymer/GDNFR protein (or variant) conjugate, with the remainder of observable molecules being unreacted (i.e., protein lacking the polymer moiety). It is also envisioned that the GDNFR protein product may involve the preparation of a pegylated molecule involving a fusion protein or linked GDNFR and GDNF molecules.

For the present reductive alkylation, the reducing agent should be stable in aqueous solution and preferably be able to reduce only the Schiff base formed in the initial process of reductive alkylation. Suitable reducing agents may be selected from sodium borohydride, sodium cyanoborohydride, dimethylamine borane, trimethylamine borane and pyridine borane. A particularly suitable reducing agent is sodium cyanoborohydride. Other reaction parameters, such as solvent, reaction times, temperatures, etc., and means of purification of products, can be determined

case-by-case based on the published information relating to derivatization of proteins with water soluble polymers (see the publications cited herein).

C. GDNFR Protein Product Pharmaceutical Compositions

5 GDNFR protein product pharmaceutical compositions typically include a therapeutically or prophylactically effective amount of GDNFR protein product in admixture with one or more pharmaceutically and physiologically acceptable formulation materials selected for suitability with the mode of administration. Suitable formulation materials include, but are not limited to, antioxidants, preservatives,
10 coloring, flavoring and diluting agents, emulsifying agents, suspending agents, solvents, fillers, bulking agents, buffers, delivery vehicles, diluents, excipients and/or pharmaceutical adjuvants. For example, a suitable vehicle may be water for injection, physiological saline solution, or artificial cerebrospinal fluid, possibly supplemented with other materials common in compositions for parenteral administration. Neutral
15 buffered saline or saline mixed with serum albumin are further exemplary vehicles. The term "pharmaceutically acceptable carrier" or "physiologically acceptable carrier" as used herein refers to a formulation material(s) suitable for accomplishing or enhancing the delivery of the GDNFR protein product as a pharmaceutical composition.

20 The primary solvent in a vehicle may be either aqueous or non-aqueous in nature. In addition, the vehicle may contain other formulation materials for modifying or maintaining the pH, osmolarity, viscosity, clarity, color, sterility, stability, rate of dissolution, or odor of the formulation. Similarly, the vehicle may contain additional formulation materials for modifying or maintaining the rate of release of GDNFR
25 protein product, or for promoting the absorption or penetration of GDNFR protein product across the blood-brain barrier.

Once the therapeutic pharmaceutical composition has been formulated, it may be stored in sterile vials as a solution, suspension, gel, emulsion, solid, or dehydrated or lyophilized powder. Such formulations may be stored either in a ready to use form
30 or in a form (e.g., lyophilized) requiring reconstitution prior to administration.

The optimal pharmaceutical formulation will be determined by one skilled in the art depending upon the intended route of administration and desired dosage. See for example, Remington's Pharmaceutical Sciences, 18th Ed. (1990, Mack Publishing Co., Easton, PA 18042) pages 1435-1712, the disclosure of which is hereby
35 incorporated by reference. Such compositions may influence the physical state, stability, rate of in vivo release, and rate of in vivo clearance of the present proteins and derivatives.

Effective administration forms, such as (1) slow-release formulations, (2) inhalant mists, or (3) orally active formulations are envisioned. The GDNFR protein product pharmaceutical composition also may be formulated for parenteral administration. Such parenterally administered therapeutic compositions are typically in the form of a pyrogen-free, parenterally acceptable aqueous solution comprising the GDNFR protein product in a pharmaceutically acceptable vehicle. One preferred vehicle is physiological saline. The GDNFR protein product pharmaceutical compositions also may include particulate preparations of polymeric compounds such as polylactic acid, polyglycolic acid, etc. or into liposomes. Hyaluronic acid may also be used, and this may have the effect of promoting sustained duration in the circulation.

A particularly suitable vehicle for parenteral injection is sterile distilled water in which the GDNFR protein product is formulated as a sterile, isotonic solution, properly preserved. Yet another preparation may involve the formulation of the GDNFR protein product with an agent, such as injectable microspheres or liposomes, that provides for the slow or sustained release of the protein which may then be delivered as a depot injection. Other suitable means for the introduction of GDNFR protein product include implantable drug delivery devices which contain the GDNFR protein product.

The preparations of the present invention may include other components, for example parenterally acceptable preservatives, tonicity agents, cosolvents, wetting agents, complexing agents, buffering agents, antimicrobials, antioxidants and surfactants, as are well known in the art. For example, suitable tonicity enhancing agents include alkali metal halides (preferably sodium or potassium chloride), mannitol, sorbitol and the like. Suitable preservatives include, but are not limited to, benzalkonium chloride, thimerosal, phenethyl alcohol, methylparaben, propylparaben, chlorhexidine, sorbic acid and the like. Hydrogen peroxide may also be used as preservative. Suitable cosolvents are for example glycerin, propylene glycol and polyethylene glycol. Suitable complexing agents are for example caffeine, polyvinylpyrrolidone, beta-cyclodextrin or hydroxypropyl-beta-cyclodextrin. Suitable surfactants or wetting agents include sorbitan esters, polysorbates such as polysorbate 80, tromethamine, lecithin, cholesterol, tyloxapal and the like. The buffers can be conventional buffers such as borate, citrate, phosphate, bicarbonate, or Tris-HCl.

The formulation components are present in concentration that are acceptable to the site of administration. For example, buffers are used to maintain the composition at physiological pH or at slightly lower pH, typically within a pH range of from about 5 to about 8.

A pharmaceutical composition may be formulated for inhalation. For example, the GDNFR protein product may be formulated as a dry powder for inhalation.

GDNFR protein product inhalation solutions may also be formulated in a liquefied propellant for aerosol delivery. In yet another formulation, solutions may be

5 nebulized.

It is also contemplated that certain formulations containing GDNFR protein product are to be administered orally. GDNFR protein product which is administered in this fashion may be formulated with or without those carriers customarily used in the compounding of solid dosage forms such as tablets and capsules. For example, a
10 capsule may be designed to release the active portion of the formulation at the point in the gastrointestinal tract when bioavailability is maximized and pre-systemic degradation is minimized. Additional formulation materials may be included to facilitate absorption of GDNFR protein product. Diluents, flavorings, low melting point waxes, vegetable oils, lubricants, suspending agents, tablet disintegrating
15 agents, and binders may also be employed.

Another preparation may involve an effective quantity of GDNFR protein product in a mixture with non-toxic excipients which are suitable for the manufacture of tablets. By dissolving the tablets in sterile water, or other appropriate vehicle, solutions can be prepared in unit dose form. Suitable excipients include, but are not
20 limited to, inert diluents, such as calcium carbonate, sodium carbonate or bicarbonate, lactose, or calcium phosphate; or binding agents, such as starch, gelatin, or acacia; or lubricating agents such as magnesium stearate, stearic acid, or talc.

Additional GDNFR protein product formulations will be evident to those skilled in the art, including formulations involving GDNFR protein product in
25 combination with GDNF protein product. Techniques for formulating a variety of other sustained- or controlled-delivery means, such as liposome carriers, bio-erodible microparticles or porous beads and depot injections, are also known to those skilled in the art. See, for example, Supersaxo et al. description of controlled release porous polymeric microparticles for the delivery of pharmaceutical compositions (International
30 Publication No. WO 93/15722; International Application No. PCT/US93/00829) the disclosure of which is hereby incorporated by reference.

D. Administration of GDNFR Protein Product

The GDNFR protein product may be administered parenterally via a variety of
35 routes, including subcutaneous, intramuscular, intravenous, transpulmonary, transdermal, intrathecal and intracerebral delivery. In addition, protein factors that do not readily cross the blood-brain barrier may be given directly intracerebrally or

otherwise in association with other elements that will transport them across the barrier. For example, the GDNFR protein product may be administered intracerebroventricularly or into the brain or spinal cord subarachnoid space. GDNFR protein product may also be administered intracerebrally directly into the brain parenchyma. GDNFR protein product may be administered extracerebrally in a form that has been modified chemically or packaged so that it passes the blood-brain barrier, or with one or more agents capable of promoting penetration of GDNFR protein product across the barrier. For example, a conjugate of NGF and monoclonal anti-transferrin receptor antibodies has been shown to be transported to the brain via binding to transferrin receptors.

To achieve the desired level of GDNFR protein product, repeated daily or less frequent injections may be administered, or GDNFR protein product may be infused continuously or periodically from a constant- or programmable-flow implanted pump. Slow-releasing implants containing the neurotrophic factor embedded in a biodegradable polymer matrix can also deliver GDNFR protein product. The frequency of dosing will depend on the pharmacokinetic parameters of the GDNFR protein product as formulated, and the route and site of administration.

Regardless of the manner of administration, the specific dose may be calculated according to body weight, body surface area or organ size. Further refinement of the calculations necessary to determine the appropriate dosage for treatment involving each of the above mentioned formulations is routinely made by those of ordinary skill in the art and is within the ambit of tasks routinely performed by them. Appropriate dosages may be ascertained through use of appropriate dose-response data.

The final dosage regimen involved in a method for treating a specific injury or condition will be determined by the attending physician. Generally, an effective amount of the present GDNFR polypeptides will be determined by considering various factors which modify the action of drugs, e.g. the age, condition, body weight, sex and diet of the patient, the severity of any infection, time of administration and other clinical factors. See, Remington's Pharmaceutical Sciences, supra, at pages 697-773, herein incorporated by reference. It is contemplated that if GDNFR is used to enhance GDNF action, then the GDNFR dose is selected to be similar to that required for GDNF therapy; if GDNFR is used to antagonize GDNF action, then the GDNFR dose would be several many times the GDNF dose. Dosing may be one or more times daily, or less frequently, and may be in conjunction with other compositions as described herein. It should be noted that the present invention is not limited to the dosages recited herein.

It is envisioned that the continuous administration or sustained delivery of

GDNFR protein products may be advantageous for a given treatment. While continuous administration may be accomplished via a mechanical means, such as with an infusion pump, it is contemplated that other modes of continuous or near continuous administration may be practiced. For example, chemical derivatization or encapsulation may result in sustained release forms of the protein which have the effect of continuous presence in the bloodstream, in predictable amounts, based on a determined dosage regimen. Thus, GDNFR protein products include proteins derivatized or otherwise formulated to effectuate such continuous administration. Sustained release forms of the GDNFR protein products will be formulated to provide the desired daily or weekly effective dosage.

It is further contemplated that the GDNFR protein product may be administered in a combined form with GDNF. Alternatively, the GDNFR and GDNF protein products may be administered separately, either sequentially or simultaneously.

GDNFR protein product of the present invention may also be employed, alone or in combination with other growth factors in the treatment of nerve disease. In addition, other factors or other molecules, including chemical compositions, may be employed together with a GDNFR protein product. In the treatment of Parkinson's Disease, it is contemplated that GDNFR protein product be used by itself or in conjunction with the administration of Levodopa, wherein the GDNFR would enhance the activity of endogenous GDNF and thereby enhance the neuronal uptake of the increased concentration of dopamine.

As stated above, it is also contemplated that additional neurotrophic or neuron nurturing factors will be useful or necessary to treat some neuronal cell populations or some types of injury or disease. Other factors that may be used in conjunction with GDNFR or a combination of GDNFR and GDNF include, but are not limited to: mitogens such as insulin, insulin-like growth factors, epidermal growth factor, vasoactive growth factor, pituitary adenylate cyclase activating polypeptide, interferon and somatostatin; neurotrophic factors such as nerve growth factor, brain derived neurotrophic factor, neurotrophin-3, neurotrophin-4/5, neurotrophin-6, insulin-like growth factor, ciliary neurotrophic factor, acidic and basic fibroblast growth factors, fibroblast growth factor-5, transforming growth factor- β , cocaine-amphetamine regulated transcript (CART); and other growth factors such as epidermal growth factor, leukemia inhibitory factor, interleukins, interferons, and colony stimulating factors; as well as molecules and materials which are the functional equivalents to these factors.

GDNFR Protein Product Cell Therapy and Gene Therapy

GDNFR protein product cell therapy, e.g., intracerebral implantation of cells producing GDNFR protein product, is also contemplated. This embodiment would involve implanting into patients cells capable of synthesizing and secreting a biologically active form of GDNFR protein product. Such GDNFR protein product-producing cells may be cells that are natural producers of GDNFR protein product or may be recombinant cells whose ability to produce GDNFR protein product has been augmented by transformation with a gene encoding the desired GDNFR protein product. Such a modification may be accomplished by means of a vector suitable for delivering the gene as well as promoting its expression and secretion. In order to minimize a potential immunological reaction in patients being administered a GDNFR protein product of a foreign species, it is preferred that the natural cells producing GDNFR protein product be of human origin and produce human GDNFR protein product. Likewise, it is preferred that the recombinant cells producing GDNFR protein product be transformed with an expression vector containing a gene encoding a human GDNFR protein product.

Implanted cells may be encapsulated to avoid infiltration of surrounding tissue. Human or non-human animal cells may be implanted in patients in biocompatible, semipermeable polymeric enclosures or membranes that allow release of GDNFR protein product, but that prevent destruction of the cells by the patient's immune system or by other detrimental factors from the surrounding tissue. Alternatively, the patient's own cells, transformed to produce GDNFR protein product *ex vivo*, could be implanted directly into the patient without such encapsulation.

Techniques for the encapsulation of living cells are familiar to those of ordinary skill in the art, and the preparation of the encapsulated cells and their implantation in patients may be accomplished without undue experimentation. For example, Baetge et al. (International Publication No. WO 95/05452; International Application No. PCT/US94/09299 the disclosure of which is hereby incorporated by reference) describe biocompatible capsules containing genetically engineered cells for the effective delivery of biologically active molecules. In addition, see U.S. Patent Numbers 4,892,538, 5,011,472, and 5,106,627, each of which is specifically incorporated herein by reference. A system for encapsulating living cells is described in PCT Application WO 91/10425 of Aebischer et al., specifically incorporated herein by reference. See also, PCT Application WO 91/10470 of Aebischer et al., Winn et al., *Exper. Neurol.*, 113:322-329, 1991, Aebischer et al., *Exper. Neurol.*, 111:269-275, 1991; Tresco et al., *ASAIO*, 38:17-23, 1992, each of which is specifically incorporated herein by reference.

In vivo and *in vitro* gene therapy delivery of GDNFR protein product is also

envisioned. In vitro gene therapy may be accomplished by introducing the gene coding for GDNFR protein product into targeted cells via local injection of a nucleic acid construct or other appropriate delivery vectors. (Hefti, J. Neurobiol., 25:1418-1435, 1994). For example, a nucleic acid sequence encoding a GDNFR protein product may be contained in an adeno-associated virus vector for delivery into the targeted cells (e.g., Johnson, International Publication No. WO 95/34670; International Application No. PCT/US95/07178 the disclosure of which is hereby incorporated by reference). Alternative viral vectors include, but are not limited to, retrovirus, adenovirus, herpes simplex virus and papilloma virus vectors. Physical transfer, either in vivo or ex vivo as appropriate, may also be achieved by liposome-mediated transfer, direct injection (naked DNA), receptor-mediated transfer (ligand-DNA complex), electroporation, calcium phosphate precipitation or microparticle bombardment (gene gun).

It is also contemplated that GDNFR protein product gene therapy or cell therapy can further include the delivery of GDNF protein product. For example, the host cell may be modified to express and release both GDNFR protein product and GDNF protein product. Alternatively, the GDNFR and GDNF protein products may be expressed in and released from separate cells. Such cells may be separately introduced into the patient or the cells may be contained in a single implantable device, such as the encapsulating membrane described above.

It should be noted that the GDNFR protein product formulations described herein may be used for veterinary as well as human applications and that the term "patient" should not be construed in a limiting manner. In the case of veterinary applications, the dosage ranges may be determined as described above.

EXAMPLES

30

Example 1

Identification of Cells Expressing High Affinity GDNF Binding Sites

Expression cloning involved the selection of a source of mRNA which is likely to contain significant levels of the target transcript. Retina photoreceptor cells were identified as responsive to GDNF at very low concentrations, suggesting the existence of a functional, high affinity receptor. To confirm that rat photoreceptor cells did express a high affinity receptor for GDNF, [¹²⁵I]GDNF binding and photographic

emulsion analysis were carried out.

Rat Retinal Cell Cultures

The neural retinas of 5-day-old C57Bl/6 mouse pups or 3-day-old Sprague-Dawley rat pups (Jackson Laboratories, Bar Harbor, MA) were carefully removed and dissected free of the pigment epithelium, cut into 1 mm² fragments and placed into ice-cold phosphate-buffered saline (PBS). The retinas were then transferred into 10 mL of Hank's balanced salt solution (HBSS) containing 120 units papain and 2000 units DNAase and incubated for 20 minutes at 37°C on a rotary platform shaker at about 200 rpm. The cells were then dispersed by trituration through fire-polished Pasteur pipettes, sieved through a 20 µm Nitex nylon mesh and centrifuged for five minutes at 200 x g. The resulting cell pellet was resuspended into HBSS containing 1% ovalbumin and 500 units DNAase, layered on top of a 4 % ovalbumin solution (in HBSS) and centrifuged for 10 minutes at 500 x g. The final pellet was resuspended in complete culture medium (see below), adjusted to about 15,000 cells/mL, and seeded in 90 µl aliquots into tissue culture plates coated with polyornithine and laminin as previously described (Louis et al., Journal Of Pharmacology And Experimental Therapeutics, 262, 1274-1283, 1992).

The culture medium consisted of a 1:1 mixture of Dulbecco's Modified Eagle's Medium (DMEM) and F12 medium, and was supplemented with 2.5% heat-inactivated horse serum (Hyclone, Logan, UT), B27 medium supplement (GIBCO, Grand Island, NY), D-glucose (final concentration: 5mg/mL), L-glutamine (final concentration: 2mM), 20 mM HEPES, bovine insulin and human transferrin (final concentrations: 2.5 and 0.1 mg/mL, respectively).

Immunocytochemical identification of photoreceptors

Photoreceptors were identified by immunostaining for arrestin, a rod-specific antigen. Cultures of photoreceptors were fixed for 30 minutes at room temperature with 4% paraformaldehyde in PBS, pH 7.4, followed by three washes in PBS. The fixed cultures were then incubated in Superblock blocking buffer (Pierce, Rockford, IL), containing 1% Nonidet P-40 to increase the penetration of the antibodies. The anti-arrestin antibodies (polyclonal rabbit antibody against the synthetic peptide sequence of arrestin: Val-Phe-Glu-Glu-Phe-Ala-Arg-Gln-Asn-Leu-Lys-Cys) were then applied at a dilution of between 1:2000 in the same buffer, and the cultures were incubated for one hour at 37°C on a rotary shaker. After three washes with PBS, the cultures were incubated for one hour at 37°C with goat-anti-rabbit IgG (Vectastain kit from Vector Laboratories, Burlingame, CA) at a 1:500 dilution. After three washes

with PBS, the secondary antibodies were then labeled with an avidin-biotin-peroxidase complex diluted at 1:500 (45 minutes at 37°C). After three more washes with PBS, the labeled cell cultures were reacted for 5-20 minutes in a solution of 0.1 M Tris-HCl, pH 7.4, containing 0.04% 3',3'-diaminobenzidine-(HCl)₄, 0.06 percent NiCl₂ and
5 0.02 percent hydrogen peroxide. Based on arrestin-immunoreactivity, about 90% of the cells in the cultures were rod photoreceptors.

The survival of photoreceptors was determined by examination of arrestin-stained cultures with bright-light optics at 200X magnification. The number of arrestin-positive photoreceptors was counted in one diametrical 1 X 6 mm strip,
10 representing about 20 percent of the total surface area of a 6 mm-well. Viable photoreceptors were characterized as having a regularly-shaped cell body, with a usually short axon-like process. Photoreceptors showing signs of degeneration, such as having irregular, vacuolated perikarya or fragmented neurites, were excluded from the counts (most of the degenerating photoreceptors, however, detached from the
15 culture substratum). Cell numbers were expressed either as cells/6-mm well.

Cultured rat retinal cells enriched for photoreceptors (10,000/6-mm well) were treated with human recombinant GDNF (ten-fold serial dilutions ranging from 10 ng/mL to 1 pg/mL). The cultures were fixed after six days and immunostained for
20 arrestin, a rod photoreceptor-specific antigen. In cultures that were not treated with GDNF, the number of photoreceptors declined steadily over time to reach about 25 percent of the initial number after six days in culture. Treatment of the cultures with GDNF resulted in an about two-fold higher number of viable arrestin-positive photoreceptors after six days in culture. The effect of GDNF was maximal at about
25 200 pg/mL, with an ED₅₀ of about 30 pg/mL. In addition to promoting photoreceptor survival, the addition of the GDNF also stimulated the extension of their axon-like process, thereby demonstrating an effect on the morphological development of the photoreceptors (mean neurite length of photoreceptors in GDNF: 68 μ m, compared to 27 \pm 18 μ m in control cultures).

30 In order to confirm that rat retinal cells express high affinity GDNF receptors, [¹²⁵I]GDNF binding and photographic emulsion analysis were carried out. Post-natal rat photoreceptor cells were seeded on plastic slide flaskettes (Nunc) at a density of 2800 cells/mm², three to four days before the experiments. The cells were washed once with ice-cold washing buffer (Dulbecco's Modified Eagle's Medium (DMEM)
35 containing 25 mM N-2-hydroxyethylpiperazine-N'-2-ethanesulfonic acid (HEPES), pH 7.5). For competitive binding, the cells were incubated with various concentrations of [¹²⁵I]GDNF in binding buffer (DMEM containing 25 mM HEPES,

pH 7.5, and 2 mg/mL of bovine serum albumin (BSA)) in the presence or absence of 500 nM unlabeled GDNF at 4°C for four hours. Cells were washed four times with ice-cold washing buffer, lysed in 1 M NaOH and the radioactivity associated with the cells was determined in a gamma counter. A significant amount of [¹²⁵I]GDNF
5 bound to the photoreceptor cells even at low ligand concentrations (as low as 30 pM), and this binding was inhibited completely by the presence of excess unlabeled GDNF.

For photographic emulsion detection, cells were incubated with 50 pM of [¹²⁵I]GDNF in binding buffer in the presence or absence of 500 nM unlabeled GDNF at 4°C for four hours. Cells were washed six times with ice-cold washing buffer,
10 fixed with 2.5% glutaraldehyde and dehydrated sequentially with 50% and 70% ethanol, and dipped in NTB-2 photographic emulsion (Eastman Kodak, Rochester NY). After five days of exposure, the slides were developed and examined. The photographic emulsion analysis demonstrated the association of [¹²⁵I]GDNF to some of the photoreceptor cells, thereby indicating the presence of a receptor for GDNF.
15 This association, however, was efficiently blocked by the addition of unlabeled GDNF.

Example 2

20 Expression Cloning of a GDNFR from Photoreceptor Cells

Rat photoreceptor cells were selected as a possible source of a high affinity receptor for GDNF based upon their cell surface binding of radiolabeled GDNF and their ability to respond to very low concentrations of the ligand, as described in
25 Example 1. In order to identify the receptor, a size-selected cDNA library of approximately 50,000 independent clones was constructed using a mammalian expression vector (a derivative of pSR, Takebe et al., 1988 supra) and mRNA isolated from cultured post-natal rat photoreceptor cells, by the methods described below. The library was divided into pools of approximately 1,500 to 2,000 independent clones
30 and screened using an established expression cloning approach (Gearing et al., EMBO Journal, 8, 3667-3676, 1989). Plasmid DNA representing each pool of the library was prepared and transfected into COS7 cells grown on plastic microscope slide flaskettes (Nunc, Naperville, IL).

The transfected cells were treated with [¹²⁵I]GDNF, fixed with
35 glutaraldehyde, dehydrated, and dipped in photographic emulsion for autoradiography. Following exposure for five days, the slides were developed and examined for the presence of cells covered by silver grains which indicated the binding

of [125 I]GDNF to the cell surface as a result of the cell's expression of a receptor for GDNF. EGF receptor transfected cells treated with [125 I]EGF were used as a positive control.

One of the 27 pools (F8-11) screened in this manner exhibited 19 positive cells following transfection. Thus, a single cDNA library pool was identified which contained a cDNA clone that expressed GDNFR. This pool was divided into 60 smaller subpools of 100 clones/pool which were rescreened by the same procedure described above. Five of these pools were identified as positive and two of the five pools were further subdivided to yield single clones responsible for the GDNF binding activity. Transfection of plasmid DNA from the single clones into COS7 cells resulted in the binding of [125 I]GDNF to approximately 15% of the cells. This binding was specifically inhibited by competition with excess unlabeled GDNF.

Construction of Expression cDNA Libraries

Rat retinal cells were harvested from postnatal day 3-7 rats and seeded into culture dishes coated with laminin and polyornithine at a density of approximately 5700 cells/mm². After 3-4 days in culture, the population was estimated to contain approximately 80% photoreceptor cells. Total RNA was prepared from this culture by standard methods, and Poly A+ RNA was purified using a polyA-tract kit (Promega, Madison, WI). A cDNA library was constructed from the rat photoreceptor poly A+ RNA using the Gibco Superscript Choice System (Gibco/BRL, Gaithersburg, MD). Two micrograms of poly A+ RNA were mixed with 50 ng of random hexamers, heated to 70°C for 10 minutes and then quick-chilled on ice. First strand synthesis was carried out with 400U Superscript II RT at 37°C for one hour. Second strand synthesis was performed in the same tube after the addition of dNTPs, 10U of E. coli DNA ligase, 40U of E. coli DNA polymerase I, and 2U of E. coli RNase H. After two hours at 16°C, the cDNA ends were blunted by treatment with 10U of T4 polymerase for an additional five minutes at 16°C. Following isopropanol precipitation, EcoRI cloning sites were added to the cDNA by ligation overnight with 10 µg of unphosphorylated EcoRI adapter oligonucleotides.

The EcoRI adapted cDNA was then phosphorylated and applied to a Sephacryl S-500 HR size fractionation column. Following loading, the column was washed with 100 µl aliquots of TEN buffer (10 mM Tris-HCl pH 7.5, 0.1 mM EDTA, 25 mM NaCl), and 30 µl fractions were collected. Fractions 6 through 8, which contained approximately 34 ng of high molecular weight cDNA, were pooled and precipitated. The recovered EcoRI-adapted cDNA was ligated overnight with 50 ng of EcoRI cut vector pBJ5. Aliquots of the ligation mix containing about 15 ng cDNA

each were transformed into competent cells (E. coli strain DH10B; GIBCO/BRL, Gaithersburg, MD) by electroporation. The transformation mixture was titered and then plated on 27 Amp/LB plates at a density of 1500 colonies/plate. Colonies were scraped from each plate and collected into 10 mL of Luria broth (LB) to make 27 pools of 1500 independent clones each. A portion of the cells from each pool was frozen in glycerol and the remainder was used to isolate plasmid DNA using a Qiagen tip-500 kit (Qiagen Inc., Chatsworth, CA).

COS Cell Transfection and Photographic Emulsion Analysis

COS7 cells were seeded (220,000 cells/slide) on plastic slide flaskettes (Nunc) coated with ProNectin (10 µg/mL in phosphate buffered saline (PBS)) one day before transfection. For transfection, 700 µl of Opti MEMI (GIBCO/BRL, Gaithersburg, MD) containing 2 µg cDNA was mixed gently with 35 µl of DEAE Dextran solution (10 mg/mL, Sigma, St. Louis, MO) in an Eppendorf tube. Cells were washed twice with PBS and incubated with the transfection mix for 30 minutes at 37°C in a 5% CO₂ atmosphere. Following incubation, 3 mL of DMEM media containing 10% fetal calf serum (FCS) and 80 nM Chloroquine (Sigma, St. Louis, MO) were added to each flaskette. Cells were further incubated for 3.5 hours, shocked with 10% dimethylsulfoxide in DMEM at room temperature for two minutes, washed once with PBS, and allowed to grow in DMEM containing 10% FCS. After 48 hours, the transfected COS7 cells were washed once with ice-cold washing buffer (DMEM containing 25 mM HEPES, pH 7.5) and incubated in ice-cold binding buffer (DMEM containing 25 mM HEPES, pH 7.5 and 2 mg/mL BSA) supplemented with 50 pM [¹²⁵I]GDNF at 4°C for four hours. Cells were washed six times in ice-cold washing buffer, fixed with 2.5% glutaraldehyde at room temperature for five minutes, dehydrated sequentially with 50% and 70% ethanol, and then dipped in NTB-2 photographic emulsion (Eastman Kodak). After 4-5 day exposure at 4°C in dark, the slides were developed and screened by bright-field and dark-field microscopy.

Subdivision of Positive Pools

A single pool was identified which contained a putative GDNF receptor clone. Clones from this pool were plated on 60 plates at a density of 100 colonies/plate. Cells were scraped from each plate, collected in LB, and allowed to grow for 4-5 hours at 37°C. Frozen stocks and DNA preparations were made from each pool, as before, to generate 60 subpools containing 100 independent clones each. Two of these 60 subpools were identified as positive by the method described above, and clones from those pools were plated at low density to allow isolation of single

colonies. Single colonies (384) were picked from each of the two subpools and grown for six hours in 200 µl LB in 96-well plates. In order to select single clones expressing GDNFR, the four 96-well plates were arrayed into a single large matrix consisting of 16 rows and 24 columns. Cells from the wells in each row and in each column were combined to yield a total of 40 mixtures. These mixtures were grown overnight in 10 mL LB/Amp (100 µg/mL), and DNA was prepared using a Qiagen tip-20 kit. When analyzed for putative GDNF receptor clones, three row mixtures and three column mixtures gave positive signals, suggesting nine potentially positive single clones. DNA from each of the potentially positive single clones was prepared and digested with EcoRI and PstI. DNA from three of the nine single clones exhibited identical restriction patterns while the other six were unrelated, suggesting that the three represented the authentic clones containing GDNFR.

15

Example 3

DNA Sequencing and Sequence Analysis

DNA from positive, single clones was prepared and sequenced using an automated ABI373A DNA sequencer (Perkin/Elmer Applied Biosystems, Santa Clara, CA) and dideoxy-dye-terminators, according to manufacturer's instructions. Comparison of GDNF receptor sequence with all available public databases was performed using the FASTA (Pearson and Lipman, Proceedings Of The National Academy Of Sciences U.S.A., 85, 2444-2448, 1988) program algorithm as described in the University of Wisconsin Genetics Computer Group package (Program Manual for the Wisconsin Package, Version 8, September 1994, Genetics Computer Group, Madison, Wisconsin).

Sequence Characterization of the Rat GDNFR

Plasmid DNA from the clones described in Example 2, above, was prepared and submitted for DNA sequence analysis. Nucleotide sequence analysis of the cloned 2138 bp rat cDNA revealed a single large open reading frame encoding a translation protein of 468 amino acid residues (Figure 3).

The coding sequence is flanked by a 5'-untranslated region of 301 bp and a 3'-untranslated region of 430 bp that does not contain a potential polyadenylation site. The presence of an in-frame stop codon upstream of the first ATG at base pair 302 and its surrounding nucleotide context indicate that this methionine codon is the most likely translation initiator site (Kozak, Nucleic Acids Research. 15, 8125-8148, 1987).

No polyadenylation signal is found in the 430 nucleotides of 3' untranslated sequence in the rat cDNA clone. This is not surprising, since the Northern blot data shows the shortest mRNA transcripts to be approximately 3.6 kb.

5 The GDNFR polypeptide sequence has an N-terminal hydrophobic region of approximately 19 residues (methionine-1 to alanine-19, Figure 3) with the characteristics of a secretory signal peptide (von Heijne, Protein Sequences And Data Analysis. 1, 41-42, 1987; von Heijne, Nucleic Acids Research. 14, 4683-4690, 1986). No internal hydrophobic domain that could serve as a transmembrane domain was found. Instead, a carboxy-terminal hydrophobic region of 21 residues (leucine-10 448 to serine-468 in Figure 3) is present and may be involved in a glycosyl-phosphatidylinositol (GPI) anchorage of the receptor to the cytoplasmic membrane. Except for the presence of three potential N-linked glycosylation sites, no conserved sequence or structural motifs were found. The protein is extremely rich in cysteine (31 of the 468 amino acid residues) but their spacing is not shared with that of cysteine-rich domains found in the extracellular portions of known receptors. 15

The GDNFR sequence was compared to sequences in available public databases using FASTA. The search did not reveal significant homology to other published sequences. Once the rat cDNA clone was obtained, it was radiolabeled and used to probe a cDNA library prepared from human brain substantia nigra as described 20 below in Example 5.

Example 4

GDNF Binding to Cells Expressing GDNFR

25 A binding assay was performed in accordance with an assay method previously described by Jing et al.. (Journal Of Cell Biology, 110, 283-294, 1990). The assay involved the binding of [¹²⁵I]GDNF to rat photoreceptor cells, COS7 cells or 293T cells which had been transfected to express GDNFR. Recombinant GDNFR 30 expressed on the surface of 293T cells was able to bind GDNF specifically and with an affinity comparable to that observed for GDNF binding sites on rat retinal cells.

Rat photoreceptor cells were prepared as described in Example 1, above, and seeded at a density of 5.7×10^5 cells/cm² two to three days before the assay in 24-well Costar tissue culture plates pre-coated with polyornithine and laminin. COS7 35 cells were seeded at a density of 2.5×10^4 cells/cm² one day before the assay and transfected with 10-20 µg of plasmid DNA using the DEAE-dextran-chloroquine method (Aruffo and Seed, Proceedings Of The National Academy Of Sciences

U.S.A., 84, 8573-8577, 1987). Cells from each dish were removed and reseeded into 30 wells of 24-well Costar tissue culture plates 24 hours following the transfection, and allowed to grow for an additional 48 hours. Cells were then left on ice for 5 to 10 minutes, washed once with ice-cold washing buffer and incubated with 0.2 mL of binding buffer containing various concentrations of [125 I]GDNF with or without unlabeled GDNF at 4°C for four hours. Cells were washed four times with 0.5 mL ice-cold washing buffer and lysed with 0.5 mL of 1 M NaOH. The lysates were counted in a 1470 Wizard Automatic Gamma Counter.

For some binding experiments, transiently transfected 293T cells were used (see below for 293T cell transfection). Two days following transfection, cells were removed from dishes by 2x versine. Cells were pelleted, washed once with ice-cold binding buffer and resuspended in ice-cold binding buffer at a density of 3×10^5 cells/mL. The cell suspension was divided into aliquots containing 1.5×10^5 cell/sample. Cells were then pelleted and incubated with various concentrations of [125 I]GDNF in the presence or absence of 500 nM of unlabeled GDNF at 4°C for four hours with gentle agitation. Cells were washed four times with ice-cold washing buffer and resuspended in 0.5 mL washing buffer. Two 0.2 mL aliquots of the suspension were counted in a gamma counter to determine the amount of [125 I]GDNF associated with the cells.

In all assays, nonspecific binding was determined by using duplicate samples, one of which contained 500 nM of unlabeled GDNF. The level of nonspecific binding varied from 10% to 20% of the specific binding measured in the absence of unlabeled GDNF and was subtracted from the specific binding. The assays demonstrated that cells did not bind GDNF unless the cell had been transfected with the GDNFR cDNA clone.

Example 5

Tissue Distribution of GDNFR mRNA

The pattern of expression of GDNFR mRNA in embryonic mouse, adult mouse, rat, and human tissues was examined by Northern blot analysis. The cloned rat GDNFR cDNA was labeled using the Random Primed DNA Labeling Kit (Boehringer Mannheim, Indianapolis, IN) according to the manufacturer's procedures. Rat, mouse, and human tissue RNA blots (purchased from Clontech, Palo Alto, CA) were hybridized with the probe and washed using the reagents of the ExpressHyb Kit (Clontech) according to the manufacturer's instructions.

Tissue Northern blots prepared from adult rat, mouse, and human tissues indicated that GDNFR mRNA is most highly expressed in liver, brain, and kidney. High mRNA expression was also detected in lung, with lower or non-detectable amounts in spleen, intestine, testis, and skeletal muscle. In blots made from mRNA isolated from mouse embryo, expression was undetectable at embryonic day 7, became apparent at day E11, and was very high by day E17. GDNFR mRNA was expressed in tissue isolated from several subregions of adult human brain at relatively equal levels. Expression of GDNFR mRNA in human adult brain showed little specificity for any particular region.

In most tissues, transcripts of two distinct sizes were present. In mouse and human tissues, transcripts of 8.5 and 4.4 kb were found, while in rat the transcripts were 8.5 and 3.6 kb. The relative amounts of the larger and smaller transcripts varied with tissue type, the smaller transcript being predominant in liver and kidney and the larger being more abundant in brain. The binding of GDNF to 293T cells transfected with a GDNFR cDNA clone in the pBKRSV vector was examined by Scatchard analysis. Two classes of binding sites were detected, one with a binding affinity in the low picomolar range and another with an affinity of about 500 pM.

20

Example 6

Recombinant Human GDNFR

An adult human substantia nigra cDNA library (5'-stretch plus cDNA library, Clontech, Palo Alto, CA) cloned in bacteriophage gt10 was screened using the rat GDNFR cDNA clone of Example 1 as a probe. The probe was labeled with [³²P]-dNTPs using a Random Primed DNA Labeling Kit (Boehringer Mannheim, Indianapolis, IN) according to the manufacturer's instructions. Approximately 1.2×10^6 gt10 phage from the human substantia nigra cDNA library were plated on 15 cm agarose plates and replicated on duplicate nitrocellulose filters. The filters were then screened by hybridization with the radiolabeled probe. The filters were prehybridized in 200 mL of 6 x SSC, 1 x Denhardt's, 0.5% SDS, 50 µg/mL salmon sperm DNA at 55°C for 3.5 hours. Following the addition of 2×10^8 cpm of the radiolabeled probe, hybridization was continued for 18 hours. Filters were then washed twice for 30 minutes each in 0.5x SSC, 0.1% SDS at 55°C and exposed to X-ray film overnight with an intensifying screen.

Five positive plaques were isolated whose cDNA inserts represented portions of the human GDNFR cDNA. In comparison to the nucleic acid sequence of rat

GDNFR depicted in Figure 3 (bp 0 through 2140), the five human GDNFR clones were found to contain the following sequences:

TABLE 3

Clone 2	1247 through 2330 (SEQ ID NO:21)
Clone 9	1270 through 2330 (SEQ ID NO:23)
Clone 21-A	-235 through 1692 (SEQ ID NO:9)
Clone 21-B	-237 through 1692 (SEQ ID NO:11)
Clone 29	805 through 2971 (SEQ ID NO:15)

An alignment and comparison of the sequences, as depicted in Figure 5, provided a consensus sequence for human GDNFR. The translation product predicted by the human cDNA sequence consists of 465 amino acids and is 93% identical to rat GDNFR.

To generate a human cDNA encoding the full length GDNFR, portions of clones 21B and 2 were spliced together at an internal BglII site and subcloned into the mammalian expression vector pBKRSV (Stratagene, La Jolla, CA).

Recombinant human GDNFR expression vectors may be prepared for expression in mammalian cells. As indicated above, expression may also be in non-mammalian cells, such as bacterial cells. The nucleic acid sequences disclosed herein may be placed into a commercially available mammalian vector (for example, CEP4, Invitrogen) for expression in mammalian cells, including the commercially available human embryonic kidney cell line, "293". For expression in bacterial cells, one would typically eliminate that portion encoding the leader sequence (e.g., nucleic acids 1-590 of Figure 1). One may add an additional methionyl at the N-terminus for bacterial expression. Additionally, one may substitute the native leader sequence with a different leader sequence, or other sequence for cleavage for ease of expression.

Example 7

Soluble GDNFR Constructs

Soluble human GDNFR protein products were made. The following examples provide four different forms, differing only at the carboxy terminus, indicated by residue numbering as provided in Figure 2. Two are soluble forms truncated at different points just upstream from the hydrophobic tail and downstream from the last

cysteine residue. The other two are the same truncations but with the addition of the "FLAG" sequence, an octapeptide to which a commercial antibody is available (Eastman Kodak). The FLAG sequence is H2N- DYKDDDDK - COOH.

5 Method

Lambda phage clone #21, containing nearly the entire coding region of human GDNFR, was digested with EcoRI to excise the cDNA insert. This fragment was purified and ligated into EcoRI cut pBKRSV vector (Stratagene, La Jolla, CA) to produce the clone 21-B-3/pBKRSV. Primers 1 and 2 as shown below were used in a
 10 PCR reaction with the human GDNFR clone 21-B-3/pBKRSV as template. PCR conditions were 94°C, five minutes followed by 25 cycles of 94°C, one minute; 55°C, one minute; 72°C, two minutes and a final extension of five minutes at 72°C. This produced a fragment consisting of nucleotides 1265-1868 of the human GDNFR clone plus a termination codon and Hind III restriction site provided by primer 2. This
 15 fragment was digested with restriction enzymes Hind III (contained in primer 2) and BglII (position 1304 in human GDNFR), and the resulting 572 nucleotide fragment was isolated by gel electrophoresis. This fragment contained the hGDNFR- coding region from isoleucine-255 to glycine-443. A similar strategy was used with primers 1 and 3 to produce a fragment with BglII and HindIII ends which coded for
 20 isoleucine-255 to proline-446. Primers 4 and 5 were designed to produce fragments coding for the same regions of hGDNFR and primers 1 and 3, but with the addition of the Flag peptide coding sequence (IBI/Kodak, New Haven, CN). The Flag peptide sequence consists of eight amino acids (H2N-Asp-Tyr-Lys-Asp-Asp-Asp-Asp-Lys-COOH) to which antibodies are commercially available. Primers 1 and 4 or 1 and 5
 25 were used in PCR reactions with the same template as before, and digested with HindIII and BglII as before. This procedure produced fragments coding for isoleucine-255 to glycine-443 and isoleucine-255 to proline-446, but with the addition of the Flag peptide at their carboxy termini.

30 Primers

- 1) 5'-CTGTTTGAATTTGCAGGACTC-3' (SEQ ID NO:30)
- 2) 5'-CTCCTCTCTAAGCTTCTAACCACAGCTTGGAGGAGC-3' (SEQ ID NO:31)
- 3) 5'-CTCCTCTCTAAGCTTCTATGGGCTCAGACCACAGCTT-3' (SEQ ID NO:32)
- 4) 5'-CTCCTCTCTAAGCTTCTACTTGTTCATCGTCGTCCTTGTAGTCACCACAGCTTGGAGGAGC-3' (SEQ ID NO:33)
- 35 5) 5'-CTCCTCTCTAAGCTTCTACTTGTTCATCGTCGTCCTTGTAGTCTGGCTCAGACCACAGCTT-3' (SEQ ID NO:34)

All four fragments, produced as described above, were transferred back into 21B3/pBKRSV. The 21B3/pBKRSV clone was digested with BglII and HindIII, and treated with calf intestinal alkaline phosphatase (CIAP). The large fragment containing the vector and the human GDNFR coding region up to the BglII site was gel purified and extracted from gel. Each of the four BglII/HindIII fragments produced as described above were ligated into this vector resulting in the following constructs in the pBKRSV vector:

10

TABLE 4

- | | |
|------------------------------|--|
| 1) GDNFR/gly-443/pBKRSV | hGDNFR terminating at glycine 443, followed by stop codon |
| 2) GDNFR/pro-446/pBKRSV | hGDNFR terminating at proline 446, followed by stop codon |
| 3) GDNFR/gly-443/Flag/pBKRSV | hGDNFR terminating at glycine 443 with C-term Flag tag, followed by stop codon |
| 4) GDNFR/pro-446/Flag/pBKRSV | hGDNFR terminating at proline 446 with C-term Flag tag, followed by stop codon |

Correct construction of all clones was confirmed by DNA sequencing. Inserts from the pBKRSV clones were transferred to other expression vectors using enzyme sites present in the pBKRSV polylinker sequence as described below. Soluble GDNFRs (e.g., sGDNFR/gly and sGDNFR/pro) have also been transferred into vectors for transient expression and into pDSR-2 for stable expression in CHO cells.

pDSR α 2+PL clones:

The appropriate pBKRSV clone is digested with XbaI and SalI. The insert is ligated to pDSR α 2+PL cut with the same enzymes and treated with CIAP. This construction may be used for stable expression of GDNFR in CHO cells.

pCEP4 clones:

The appropriate pBKRSV clone is digested with SpeI and XhoI. The insert is ligated to pCEP4 (Invitrogen, San Diego, CA) digested with NheI (SpeI ends) and XhoI, and treated with CIAP. This construction may be used for transient of expression of GDNFR.

The plasmid construct pDSR-2 is prepared substantially in accordance with the process described in the co-owned and copending U. S. Patent Application Serial Number 501,904 filed March 29, 1990 (also see, European Patent Application No. 90305433, Publication No. EP 398 753, filed May 18, 1990 and WO 90/14363 (1990), the disclosures of which are hereby incorporated by reference. It will be appreciated by those skilled in the art that a variety of nucleic acid sequences encoding GDNFR analogs may be used.

Another construct is pDSR α 2, a derivative of the plasmid pCD (Okayama & Berg, Mol. Cell Biol. 3: 280-289, 1983) with three main modifications: (i) the SV40 polyadenylation signal has been replaced with the signal from the α -subunit of bovine follicular stimulating hormone, α -bFSH (Goodwin et al., Nucleic Acids Res. 11: 6873-6882, 1983); (ii) a mouse dihydrofolate reductase minigene (Gasser et al., Proc. Natl. Acad. Sci. 79: 6522-6526, 1982) has been inserted downstream from the expression cassette to allow selection and amplification of the transformants; and (iii) a 267 bp fragment containing the "R-element" and part of the "U5" sequences of the long terminal repeat (LTR) of human T-cell leukemia virus type I (HTLV-I) has been cloned and inserted between the SV40 promoter and the splice signals as described previously (Takebe et al., Mol. Cell Biol. 8: 466-472, 1988).

The expression of GDNFR in CHO cells has been verified by the binding of iodinated GDNF to the cell surface. As discussed above, the recombinantly expressed soluble GDNFR protein product may be used to potentiate the activity or cell specificity of GDNF. Soluble GDNFR attached to a detectable label also may be used in diagnostic applications as discussed above.

25

Example 8

Chemical Crosslinking of GDNF with GDNFR

In order to study its binding properties and molecular characteristics, GDNFR was transiently expressed on the surface of 293T cells by transfection of the rat cDNA clone. Transfection of 293T cells was performed using the Calcium Phosphate Transfection System (GIBCO/BRL, Gaithersburg, MD) according to the manufacturers instructions. Two days following transfection, cells were removed by 2x versine treatment, washed once with washing buffer, and resuspended in washing buffer at a density of 2×10^6 cells/mL. A duplicate set of cells were incubated with 0.5 μ M PI-PLC at 37°C for 30 minutes before [125 I]GDNF binding. These cells were washed three times with ice-cold binding buffer and then incubated with 1 to 3

nM of [125 I]GDNF along with other cells at 4°C for four hours. Cells were washed four times with ice-cold washing buffer, resuspended in washing buffer supplemented with 1 mM of Bis suberate for crosslinking (BS³ Pierce, Rockford, IL) and incubated at room temperature for 30 minutes. Following three washes with TBS, a duplicate group of samples was treated by 0.5 u/mL of PI-PLC at 37°C for 30 minutes. These cells were pelleted and the supernatants were collected. The cells were then washed with washing buffer and lysed along with all other cells with 2x SDS-PAGE sample buffer. The cell lysates and the collected supernatants were resolved on a 7.5% SDS-PAGE.

The cell suspension was divided into aliquots containing 1.5×10^5 cell/sample. Cells were then pelleted and incubated with various concentrations of [125 I]GDNF in the presence or absence of 500 nM of unlabeled GDNF at 4°C for four hours with gentle agitation. Cells were washed four times with ice-cold washing buffer and resuspended in 0.5 mL washing buffer. Two 0.2 mL aliquots of the suspension were counted in a gamma counter to determine the amount of [125 I]GDNF associated with the cells.

Although mock transfected 293T cells did not exhibit any GDNF binding capacity, GDNFR transfected cells bound [125 I]GDNF strongly even at picomolar concentrations. This binding was almost completely inhibited by 500 nM of unlabeled GDNF, indicating a specific binding of native GDNF to the expressed receptors.

GDNFR expressed by the 293T cells can be released from the cells by treatment with phosphatidylinositol-specific phospholipase C (PI-PLC, Boehringer Mannheim, Indianapolis, IN). The treatment of transfected cells with PI-PLC prior to ligand binding almost entirely eliminated the GDNF binding capacity of the cell. Additionally, treatment of the transfected cells after cross-linking released the majority of the cross-linked products into the media. These results strongly suggest that GDNFR is anchored to the cell membrane through a GPI linkage.

Crosslinking data further indicated that the molecular weight of GDNFR is approximately 50-65 kD, suggesting that there is a low level of glycosylation. Although the major cross-linked species has a molecular mass consistent with a monomer of the receptor, a minor species with approximately the mass expected for a dimer has been found.

35

Example 9

GDNF Signaling is Mediated by a Complex of GDNFR
and the Ret Receptor Protein Tyrosine Kinase

Introduction

Mice carrying targeted null mutations in the GDNF gene exhibit various defects
5 in tissues derived from neural crest cells, in the autonomic nervous system, and in
trigeminal and spinal cord motor neurons. The most severe defects are the absence of
kidneys and complete loss of enteric neurons in digestive tract. The phenotype of
GDNF knockout mice is strikingly similar to that of the c-ret knockout animals
(Schuchardt et al. 1994), suggesting a possible linkage between the signal transduction
10 pathways of GDNF and c-ret.

The proto-oncogene c-ret was identified using probes derived from an
oncogene isolated in gene transfer experiments (Takahashi et al., Cell. 42, 581-588,
1985; Takahashi and Cooper, Mol. Cell. Biol., 7, 1378-1385, 1987). Sequence
analysis of the c-ret cDNA revealed a large open reading frame encoding a novel
15 receptor protein tyrosine kinase (PTK). The family of receptor PTKs has been
grouped into sub-families according to extracellular domain structure and sequence
homology within the intracellular kinase domain (van der Geer et al., 1994). The
unique extracellular domain structure of Ret places it outside any other known receptor
PTK sub-family; it includes a signal peptide, a cadherin-like motif, and a cysteine-rich
20 region (van Heyningen, Nature, 367, 319-320, 1994; Iwamoto et al., 1993). *In situ*
hybridization and immunohistochemical analysis showed high level expression of ret
mRNA and protein in the developing central and peripheral nervous systems and in the
excretory system of the mouse embryo (Pachnis et al., 1993; Tsuzuki et al.,
Oncogene, 10, 191-198, 1995), suggesting a role of the Ret receptor either in the
25 development or in the function of these tissues. A functional ligand of the Ret receptor
has not been identified, thereby limiting a further understanding of the molecular
mechanism of Ret signaling. Mutations in the c-ret gene are associated with inherited
predisposition to cancer in familial medullary thyroid carcinoma (FMTC), and multiple
endocrine neoplasia type 2A (MEN2A) and 2B (MEN2B). These diseases are
30 probably caused by "gain of function" mutations that constitutively activate the Ret
kinase (Donis-Keller et al., Hum. Molec. Genet. 2, 851-856, 1993; Hofstra et al.,
Nature. 367, 375-376, 1994; Mulligan et al., Nature. 363, 458-460, 1993; Santoro et
al., Science. 267, 381-383, 1995). They confer a predisposition to malignancy
specifically in tissues derived from the neural crest, where ret is normally expressed in
35 early development. Another ret-associated genetic disorder, Hirschsprung's disease
(HSCR), is characterized by the congenital absence of parasympathetic innervation in
the lower intestinal tract (Edery et al., Nature. 367, 378-380, 1994; Romeo et al.,

1994). The most likely causes of HSCR are nonsense mutations that result in the production of truncated Ret protein lacking a kinase domain or missense mutations that inactivate the Ret kinase. As noted above, targeted disruption of the c-ret proto-oncogene in mice results in renal agenesis or severe dysgenesis and lack of enteric neurons throughout the digestive tract (Schuchardt et al., 1994). This phenotype closely resembles that of GDNF knockout mice. Taken together, these data suggest that both Ret and GDNF are involved in signal transduction pathways critical to the development of the kidney and the enteric nervous system. How Ret and GDNF are involved, however, was not known.

10 The isolation and characterization of cDNA for GDNFR by expression cloning, as described above, lead to the expression of GDNFR in the transformed human embryonic kidney cell line 293T. Transformation resulted in the appearance of both high (K_d of approximately 2 pM) and low (K_d of approximately 200 pM) affinity binding sites. The high affinity binding sites could be composed of homodimers or
15 homo-oligomers of GDNFR alone, or of heterodimers or hetero-oligomers of GDNFR with other molecules. As discussed above, because GDNFR lacks a cytoplasmic domain, it must function through one or more accessory molecules in order to play a role in GDNF signal transduction. In this study we confirm that, in the presence of GDNFR, GDNF associates with the Ret protein tyrosine kinase receptor, and quickly
20 induces Ret autophosphorylation.

Results

Neuro-2a Cells Expressing GDNFR Bind GDNF with High Affinity

25 Neuro-2a is a mouse neuroblastoma cell line that endogenously expresses a high level of Ret protein (Ikeda et al., *Oncogene*. 5, 1291-1296, 1990; Iwamoto et al., *Oncogene*. 8, 1087-1091, 1993; Takahashi and Cooper, 1987) but does not express detectable levels of GDNFR mRNA as judged by Northern blot. In order to determine if Ret could associate with GDNF in the presence of GDNFR, a study was performed
30 to examine the binding of [125 I]GDNF to Neuro-2a cells engineered to express GDNFR. Neuro-2a cells were transfected with a mammalian expression vector containing the rat GDNFR cDNA (such as the expression plasmid described above). Three clonal lines, NGR-16, NGR-33, and NGR-38 were tested for their ability to bind [125 I]GDNF. The unbound [125 I]GDNF was removed at the end of the
35 incubation and the amount of radioactivity associated with the cells was determined as described in Experimental Procedures. All three lines were able to bind [125 I]GDNF specifically while parental Neuro-2a cells exhibited little or no [125 I]GDNF binding

(Figure 6). Binding could be effectively competed by the addition of 500 nM unlabeled GDNF. These results demonstrate that Ret receptor expressed on Neuro-2a cells is unable to bind GDNF in the absence of GDNFR and are consistent with the previous observation that GDNFR is not expressed at appreciable levels in Neuro-2a cells.

Equilibrium binding of [125 I]GDNF to NGR-38 cells was examined over a wide range of ligand concentrations (0.5 pM to 1 nM of [125 I]GDNF in the presence or absence of 500 nM of unlabeled GDNF) (see Figure 7A). Following incubation, unbound [125 I]GDNF was removed and the radioactivity associated with the cells was determined as described in Experimental Procedures. Results are depicted in Figure 7: (A) Equilibrium binding of [125 I]GDNF to NGR-38 cells (circles) and Neuro-2a cells (squares) in the presence (open circles and open squares) or absence (filled circles and filled squares) of unlabeled GDNF; (B) Scatchard analysis of [125 I]GDNF binding to NGR-38 cells. Neuro-2a cells exhibited little binding even at a concentration of 1 nM [125 I]GDNF, and this binding was not affected by the addition of excess unlabeled GDNF. Binding to NGR-38 cells was analyzed by Scatchard plot as shown in Figure 7B. Two classes of binding sites were detected, one with $K_d = 1.5 \pm 0.5$ pM and the other with $K_d = 332 \pm 53$ pM. These dissociation constants are very similar to the values obtained for the high and low affinity binding sites in 293T cells transiently expressing GDNFR, as described above.

GDNF Associates with Ret in Neuro-2a Cells Expressing GDNFR

In order to determine if the Ret receptor PTK could associate with GDNF in cells expressing GDNFR, a cross-linking experiment was carried out using NGR-38 and parental Neuro-2a cells. NGR-38 cells were incubated with [125 I]GDNF, treated with cross-linking reagent, then lysed either directly in SDS-PAGE sample buffer or in Triton X-100 lysis buffer and further immunoprecipitated with anti-Ret antibody as described in the Experimental Procedures. The immunoprecipitates were analyzed by SDS-PAGE in the absence (NR) or presence (R) of -mercaptoethanol. Lysates were treated with Ret specific antibody, immunoprecipitated, and analyzed by SDS-PAGE under reducing conditions (see Figure 8, bands are marked as follows: ~75 kD, solid triangle; ~150 kD, open triangle; ~185 kD, solid arrow; ~250 kD, asterisk; ~400kD, open arrow). The most prominent cross-linked species were at ~75 kD, and ~185 kD, with less intense bands of ~150 kD and ~250 kD. A very faint band of ~400 kD was also visible (Figure 8, lane 2). When immunoprecipitates were analyzed by non-reducing SDS-PAGE, the ~75 kD, ~150 and ~185 kD bands were present at about the same intensity as in the reducing gel, but the amount of the ~400 kD band increased

dramatically (Figure 8, lane 4). Also becoming more prominent was the band at ~250 kD.

Under both reducing and non-reducing conditions, bands of similar molecular weight but of greatly reduced intensity were observed when parental Neuro-2a cells were used instead of NGR-38 (Figure 8, lanes 1 and 3). The ~75 kD and ~150 kD species are likely to represent cross-linked complexes of GDNF and GDNFR, since species with identical molecular weights are produced by cross-linking in 293T cells that do not express Ret. Furthermore, since the molecular weight of Ret is 170 kD, any complex including Ret must be of at least this size.

The fact that these complexes are immunoprecipitated by anti-Ret antibody indicates they are products of an association between Ret and the GDNF/GDNFR complex which was disrupted under the conditions of the gel analysis. It is envisioned that the broad band at ~185 kD probably consists of one molecule of Ret (170 kD) cross-linked with one molecule of monomeric recombinant GDNF (15 kD), although some dimeric GDNF may be included. The presence of Ret in this species was confirmed by a separate experiment in which a band of the same molecular weight was observed when unlabeled GDNF was cross-linked to NGR-38 cells and the products examined by Western blot with anti-Ret antibody (data not shown).

The ~400 kD band was not reliably identified, partly due to the difficulty in estimating its molecular weight. The fact that it is prominent only under non-reducing conditions indicates that it is a disulfide-linked dimer of one or more of the species observed under reducing conditions. The most likely explanation is that it represents a dimer of the 185 kD species, although it may be a mixture of high molecular weight complexes consisting of two Ret, one or two GDNFR, and one or two GDNF molecules. The exact identity of the ~250 kD band has not yet been determined. One possibility is that it represents cross-linked heterodimers of the ~75 kD (GDNF + GDNFR) and ~185 kD (GDNF + Ret) complexes.

GDNF Stimulates Autophosphorylation of Ret in Neuro-2a Cells Expressing GDNFR

The ability of the Ret protein tyrosine kinase receptor to associate with GDNF in the presence of GDNFR led to the study of GDNF stimulation of the autophosphorylation of Ret. NGR-38 cells were treated with GDNF, lysed, and the lysates immunoprecipitated with anti-Ret antibody. The immunoprecipitates were analyzed by Western blot using an anti-phosphotyrosine antibody as described in the Experimental Procedures. When NGR-38 cells (Figure 9A, lanes 2-4) were treated with purified recombinant GDNF produced in either mammalian (CHO cells; Figure 9A, lanes 4) or E. coli cells (Figure 9A, lanes 1, 3), a strong band was

observed at 170 kD, indicating autophosphorylation of tyrosine residues on the mature form of Ret. A much weaker corresponding band was observed in GDNF-treated Neuro-2a cells (Figure 9A, lane 1). No phosphorylation was observed on the alternatively glycosylated 150 kD precursor form of Ret (Figure 9A). The induction of Ret autophosphorylation by GDNF was dosage dependent. The dose response and kinetics of GDNF-induced Ret tyrosine phosphorylation in NGR-38 cells are shown in panels B and C. In all panels, the tyrosine phosphorylated 170 kD Ret bands are indicated by solid arrows. The amount of Ret protein loaded in each lane as determined by reprobing of the immunoblot with anti-Ret antibody (Santa Cruz, C-19, Cat. #sc-167) is shown on the right side of panel A. The band at ~150 kD represents an alternately glycosylated immature form of Ret that does not autophosphorylate. As shown in Figure 9B, stimulation of Ret autophosphorylation in NGR-38 cells could be detected with 50 pg/mL of GDNF and the response was saturated at 20-50 ng/mL GDNF. The stimulation of Ret autophosphorylation by purified recombinant GDNF in NGR-38 cells over times of 0-20 minutes following treatment is shown in Figure 9C. Increased levels of Ret autophosphorylation could be observed within one minute of GDNF treatment and was maximal at 10 minutes following treatment (Figure 9C).

GDNF and Soluble GDNFR Induce Ret Autophosphorylation in Neuro-2A Cells

As discussed above, GDNFR is anchored to the cytoplasmic membrane through a GPI linkage and can be released by treatment with phosphatidylinositol-specific phospholipase C (PI-PLC). When NGR-38 cells were incubated with PI-PLC, GDNF-induced receptor autophosphorylation of Ret in these cells was abolished (Figure 10A; PI-PLC treated (lane 1) or untreated (lanes 2 and 3) NGR-38 cells were incubated with (lanes 1 and 3) or without (lane 2) GDNF and analyzed for Ret autophosphorylation by immunoblotting as described in the Experimental Procedures).

Figure 10B depicts parental Neuro-2a cells treated with (lanes 2,4,6,8) or without (lanes 1,3,5,7) GDNF in the presence (lanes 5-8) or absence (lanes 1-4) of PI-PLC/CM obtained from Neuro-2a or NGR-38 cells, as analyzed for Ret autophosphorylation by immunoblotting as described in the Experimental Procedures. NGR-38 cells treated with GDNF were used as a positive control. In both panels A and B, the autophosphorylated 170 kD Ret bands are marked by solid arrows. When conditioned medium containing soluble GDNFR released by PI-PLC treatment (PI-PLC/CM) of NGR-38 cells was added to parental Neuro-2a cells along with GDNF, autophosphorylation of the Ret receptor comparable to that obtained with GDNF treatment of NGR-38 cells was observed (Figure 10B, lanes 2 and 8). Only

background levels of Ret autophosphorylation were observed when no GDNF was added, or when conditioned media derived from PI-PLC treatment of Neuro-2a cells was tested (Figure 10B, lanes 3-7).

5 Ret-Fc Fusion Protein Blocks Ret Phosphorylation Induced by GDNF and Soluble GDNFR

To confirm that Ret phosphorylation induced by GDNF in the presence of GDNFR is the result of receptor autophosphorylation, a study was performed to determine whether a Ret extracellular domain/Immunoglobulin Fc (Ret-Fc) fusion
10 protein could block Ret activation. Because of the technical difficulty of blocking the large number of GDNF alpha receptors expressed on NGR-38 cells, Ret phosphorylation assays were performed using Neuro-2a as the target cell and culture media removed from NGR-38 cells treated with PI-PLC as a source of GDNFR. Cells were treated with mixtures including various combinations of GDNF
15 (50 ng/mL), media containing soluble GDNFR (e.g., PI-PLC/CM derived from NGR-38 cells), and different concentrations of Ret-Fc fusion protein either alone or in various combinations as indicated in Figure 11. Neuro-2a cells were treated with GDNF, media containing soluble GDNFR, Ret-Fc, or the pre-incubated mixtures. The cells were then lysed, and the lysates were analyzed for c-Ret autophosphorylation
20 by immunoprecipitation using anti-Ret antibody as described in the Experimental Procedures. The immunoprecipitates were analyzed by Western blot using an anti-phosphotyrosine antibody.

The pre-incubated mixture of GDNF and media containing soluble GDNFR induced tyrosine phosphorylation of Ret receptors expressed in Neuro-2a at a level
25 comparable to GDNF-treated NGR-38 control cells (Figure 11, lanes 7 and 2). The position of the autophosphorylated 170 kD Ret bands are marked by a solid arrow. When Ret-Fc fusion protein was included in the pre-incubated GDNF/GDNFR mixture, Ret phosphorylation was inhibited in a dose dependent manner (Figure 11, lanes 8-10). This indicated that Ret phosphorylation is a result of a GDNF/Ret
30 interaction mediated by GDNFR. In untreated Neuro-2a cells or in cells treated with any combination of GDNF or Ret-Fc fusion protein in the absence of GDNFR, only background levels of Ret phosphorylation were observed (Figure 11, lanes 3-6).

35 GDNF Induces Autophosphorylation of c-RET Expressed in Embryonic Motor Neurons

Spinal cord motor neurons are one of the major targets of GDNF action in vivo (Henderson et al., Science. 266, 1062-1064, 1994; Li et al., Proceedings Of The

National Academy Of Sciences, U.S.A. 92, 9771-9775, 1995; Oppenheim et al., Nature. 373, 344-346, 1995; Yan et al., Nature. 373, 341-344, 1995; Zurn et al., Neuroreport. 6, 113-118, 1995). To test the ability of GDNF to induce Ret autophosphorylation in these cells, embryonic rat spinal cord motor neurons were treated with (lanes 2 and 4) or without (lanes 1 and 3) 20 ng/mL GDNF followed by lysis of the cells, immunoprecipitation with anti-Ret antibody, and analysis by Western blotting with anti-phosphotyrosine antibody as described in the Experimental Procedures. In lysates of cells treated with GDNF, a band of tyrosine phosphorylated protein with a molecular mass of ~170 kD was observed (Figure 12, lane 2). No such signal was observed with cells treated with binding buffer alone (Figure 12, lane 1). When the same Western blot filter was stripped and re-probed with anti-Ret antibody (i.e., the amount of c-Ret protein loaded in each lane was determined by reprobing the immunoblot with the anti-Ret antibody), bands with the same molecular mass and similar intensities appeared in both samples (Figure 12, lanes 3 and 4). The phosphotyrosine band in GDNF-treated cells co-migrates with the Ret protein band, indicating GDNF stimulated autophosphorylation of Ret. The autophosphorylated Ret bands (lanes 1 and 2) and the corresponding protein bands (lanes 3 and 4) were marked by a solid arrow.

20

Discussion

Polypeptide growth factors elicit biological effects through binding to their cognate cell surface receptors. Receptors can be grouped into several classes based on their structure and mechanism of action. These classifications include the protein tyrosine kinases (PTKs), the serine/threonine kinases, and the cytokine receptors. Receptor PTK signaling is initiated by a direct interaction with ligand, which induces receptor dimerization or oligomerization that in turn leads to receptor autophosphorylation. The activated receptor then recruits and phosphorylates intracellular substrates, initiating a cascade of events which culminates in a biological response (Schlessinger and Ullrich, Neuron 9, 383-391, 1992). In contrast, signal transduction by serine/threonine kinase or cytokine receptors often involves formation of multi-component receptor complexes in which the ligand binding and signal transducing components are distinct. Examples are the TGF- receptor complex, a serine/threonine kinase receptor consisting of separate binding (Type II) and signaling (Type I) components and the CNTF family. CNTF, interleukin-6 (IL-6) and leukocyte inhibitory factor (LIF) share the common signaling components, gp130 and/or LIFR, in their respective receptor complexes. While the ligand specificity of

these complexes is determined by a specific binding subunit to each individual ligand, signal transduction requires association of the initial complex of ligand and ligand binding subunit with other receptor subunits which cannot bind ligand directly (Ip et al., Cell. 69, 1121-1132, 1992). In the CNTF receptor complex, the ligand binding component is CNTF receptor (CNTFR), which like GDNFR, is a GPI-anchored membrane protein. The present invention involves the description of the first example of a receptor PTK whose autophosphorylation is dependent upon association with a separate ligand-specific binding component.

The present study confirms that GDNFR, a GPI-linked membrane protein that binds to GDNF with high affinity, is required for the efficient association of GDNF with the Ret receptor PTK. In the absence of GDNFR, GDNF is unable to bind to Ret or stimulate Ret receptor autophosphorylation. In the presence of GDNFR, GDNF associates with Ret and rapidly induces Ret autophosphorylation in a dose-dependent manner. GDNFR is able to function in either membrane bound or soluble forms (Figure 11), as discussed above. GDNF concentrations of 50 pg/mL (1.7 pM) are able activate the Ret tyrosine kinase in cells expressing GDNFR. This is consistent with the dissociation constant (1.5 pM) found for the high affinity GDNF binding sites on NGR-38 cells. The rapid induction of Ret phosphorylation by GDNF (detectable one minute after treatment) and the ability of Ret-Fc to block autophosphorylation suggest that Ret is being activated directly rather than as a downstream consequence of the phosphorylation of some other receptor.

Cross-linking studies support the hypothesis that efficient association of Ret with GDNF depends on GDNFR. Cross-linking of GDNF to Ret in NGR-38 cells which express high levels of GDNFR is robust, but in parental Neuro-2a cells cross-linked products are barely detectable. Although conclusive identification of all the cross-linked complexes is difficult, the data clearly demonstrates an association of Ret with GDNF that is dependent on the presence of GDNFR, and demonstrates that GDNFR is included in some of the cross-linked products. The reason for the presence of minor cross-linked species in Neuro-2a cells is not clear. While the expression of GDNFR mRNA in Neuro-2a cells could not be detected by Northern blot, it is possible that GDNFR is expressed at very low levels in these cells.

The fact that Ret can be activated by GDNF in cultured rat embryonic spinal cord motor neurons further demonstrates the biological relevance of the Ret/GDNF interaction. These cells are a primary target of GDNF *in vivo*, and have been shown to respond to low doses of GDNF *in vitro* (Henderson et al., 1994). Stimulation of Ret phosphorylation was abolished when the motor neuron cells were pre-treated with PI-PLC (data not shown), suggesting that the activation of Ret by GDNF requires

GDNFR.

Although binding of ligand to the receptor extracellular domain is the first step in the activation of other known receptor PTKs, the present data has shown that this is not the case for GDNF and Ret. Figure 13 depicts a model for the binding of GDNF to GDNFR and Ret, and the consequent activation of the Ret PTK in response to GDNF. The initial event in this process is the binding of disulfide-linked dimeric GDNF to GDNFR in either monomeric or dimeric form. Although there is currently no direct evidence for the existence of dimeric GDNFR, when 293T cells were transfected with GDNFR cDNA, two classes of binding sites appeared. The simplest explanation for this observation is the existence of monomeric and dimeric GDNFR, each with its own ligand binding affinity. This is consistent with the finding that GDNF binding affinities are apparently unaffected by the presence of Ret. Since the present experiments do not address the question of whether dimeric GDNFR is in equilibrium with its monomer in the absence of GDNF or if dimerization is induced by GDNF binding, these possibilities are presented as alternate pathways. The complex consisting of dimeric GDNFR and dimeric GDNF can bind two molecules of Ret, forming the active signaling complex. As for other PTKs, close contact between the intracellular catalytic domains of two Ret molecules is likely to result in receptor autophosphorylation. This notion that Ret functions by this mechanism is supported by the fact that the MEN2A mutation which causes steady state dimerization of Ret results in constitutive activation of the Ret kinase (Santoro et al., 1995).

Motor neurons have been reported to respond to GDNF with an ED₅₀ of as low as 5 fM (Henderson et al., 1994). Although it is difficult to compare binding affinity with the ED₅₀ for a biological response, it is possible that very high affinity GDNF binding sites exist on these cells. Other cells, such as embryonic chick sympathetic neurons, have been reported to bind GDNF with a K_d of 1-5 nM (Trupp et al., *Journal Of Cell Biology*. 130, 137-148, 1995). It is unlikely that GDNFR is involved in a receptor complex for such low affinity sites, but a weak direct interaction between GDNF and Ret may be present.

Expression of c-ret has been observed during embryogenesis in many cell lineages of the developing central and peripheral nervous systems, including cells of the enteric nervous system (Pachnis, et al., *Development*, 119, 1005-1017, 1993; Tsuzuki et al., 1995). Outside the nervous system, c-ret expression has been detected in the Wolffian duct, ureteric bud epithelium and collecting ducts of the kidney (Pachnis, et al., *supra*; Tsuzuki et al., 1995). Ret expression has also been detected in all neuroblastoma cell lines derived from the neural crest (Ikeda et al., 1990) and from surgically resected neuroblastomas (Nagao et al., 1990; Takahashi & Cooper, 1987).

GDNF expression has been observed in both CNS and PNS, as well as in non-neuronal tissues during embryonic development. The levels of GDNF expression found in many non-neuronal tissues were higher than in the nervous system (Choi-Lundberg and Bohn, Brain Res. Dev. Brain Res. 85, 80-88, 1995). Although
5 expression of GDNFR has not been extensively studied, primary Northern blot analysis detected the presence of high levels of the GDNFR mRNA in the liver, brain, and kidney of adult rat and mouse. The similarity of the expression patterns of ret, GDNF, and GDNFR in developing nervous system and kidney is consistent with their combined action during development.

10 Mammalian kidney development has been postulated to result from reciprocal interactions between the metanephron and the developing ureter, a branch developed from the caudal part of the Wolffian duct (Saxen, Organogenesis of the kidney. Development and Cell Biology series, Cambridge University Press, Cambridge, England, 1987). While the expression of Ret has been found at the ureteric bud but
15 not in the surrounding mesenchyme in developing embryos, the expression of GDNF was detected in the undifferentiated but not adult metanephric cap of the kidney. These observations suggest that an interaction between GDNF and Ret is responsible for initiating the development of the ureteric structure. Further support for this hypothesis is provided by targeted disruptions of the GDNF and ret genes, which result in very
20 similar phenotypic defects in kidney (Schuchardt et al., Nature. 367, 380-383, 1994; Sanchez, in press). Another major phenotypic defect observed in both GDNF (-/-) and ret (-/-) knockout animals is a complete loss of the enteric neurons throughout the digestive tract. Hirschsprung's disease, a genetic disorder characterized by the congenital absence of parasympathetic innervation in the lower intestinal tract, has also
25 been linked to "loss-of-function" mutations in ret (Romeo et al., Nature. 367, 377-378, 1994. Edery et al., 1994). A later report (Angrist et al., Hum. Mol. Genet. 4, 821-830, 1995) indicated that, contrary to earlier observations, some Hirschsprung's patients do not carry mutations in ret. It is now envisioned that such patients may carry mutations in GDNF, GDNFR or some other critical component of this signaling
30 pathway.

Experimental Procedures

[¹²⁵I]GDNF Binding to Neuro-2a Cells Expressing GDNFR

35 Neuro-2a cells (ATCC #CCL 131) were transfected with an expression plasmid, as described above, using the Calcium Phosphate Transfection System (GIBCO/BRL) according to the manufacturer's directions. Transfected cells were

selected for expression of the plasmid by growth in 400 µg/mL G418 antibiotic (Sigma). G418 resistant clones were expanded and assayed for GDNFR expression by binding to [¹²⁵I]GDNF (Amersham, Inc., custom iodination, catalog #IMQ1057). Cells from each clone were seeded at a density of 3 x 10⁴ cells/cm² in duplicate wells of 24-well tissue culture plates (Becton Dickinson) pre-coated with polyornithine. Cells were washed once with ice-cold washing buffer (DMEM containing 25 mM HEPES, pH 7.5) and were then incubated with 50 pM [¹²⁵I]GDNF in binding buffer (washing buffer plus 0.2% BSA) at 4°C for four hours either in the presence or absence of 500 nM unlabeled GDNF. Cells were then washed four times with ice-cold washing buffer, lysed in 1 M NaOH, and the cell-associated radiolabel quantitated in a 1470 Wizard Automated Gamma Counter (Wallac Inc.). The amount of GDNFR expressed by individual clones was estimated by the ratio of [¹²⁵I]GDNF bound to cells in the absence and presence of unlabeled GDNF. Three clones were chosen as representatives of high, moderate, and low level expressors of GDNFR for use in binding experiments. The ratios [¹²⁵I]GDNF bound in the absence and presence of unlabeled GDNF for these clones were: NGR-38) 16:1, NGR-16) 12.8:1, and NGR-33) 8:1. Equilibrium binding of [¹²⁵I]GDNF to NGR-38 cells was carried out as described above except that concentrations of labeled GDNF ranged from 0.5 pM to 1 nM. In all assays, nonspecific binding as estimated by the amount of radiolabel binding to cells in the presence of 500 nM unlabeled GDNF was subtracted from binding in the absence of unlabeled GDNF. Binding data was analyzed by Scatchard plot.

Chemical Cross-Linking

Neuro-2a or NGR-38 cells were washed once with phosphate-buffered saline (PBS, pH 7.1), then treated for four hours at 4°C with 1 or 3 nM [¹²⁵I]GDNF in binding buffer in the presence or absence of 500 nM unlabeled GDNF. Following binding, cells were washed four times with ice-cold washing buffer and incubated at room temperature for 45 minutes with 1 mM bis suberate (BS³, Pierce) in washing buffer. The cross-linking reaction was quenched by washing the cells three times with Tris-buffered saline (TBS, pH 7.5). The cells were then either lysed directly in SDS-PAGE sample buffer (80 mM Tris HCl [pH 6.8], 10% glycerol, 1% SDS, 0.025% bromophenol blue) or in Triton X-100 lysis buffer (50 mM Hepes, pH 7.5, 1% Triton X-100, 50 mM NaCl, 50 mM NaF, 10 mM sodium pyrophosphate, 1% aprotinin (Sigma, Cat.# A-6279), 1 mM PMSF (Sigma, Cat.# P-7626), 0.5 mM Na₃VO₄ (Fisher Cat.# S454-50). The lysates were clarified by centrifugation, incubated with 5 µg/mL of anti-Ret antibody (Santa Cruz Antibody, C-19, Cat.

- #SC-167), and the resulting immunocomplexes were collected by precipitation with protein A-Sepharose CL-4B (Pharmacia). The immunoprecipitates were washed three times with the lysis buffer, once with 0.5% NP-40 containing 50 mM NaCl and 20 mM Tris-Cl, pH 7.5, and were then resuspended in SDS-PAGE sample buffer.
- 5 Both the whole cell lysates and the immunoprecipitates were fractionated by 7.5% SDS-PAGE with a ratio of Bis:Acrylamide at 1:200.

Western Blot Analysis

- The autophosphorylation of Ret receptor was examined by Western blot analysis. Briefly, cells were seeded 24 hours prior to the assay in 6-well tissue culture dishes at a density of 1.5×10^6 cells /well. Cells were washed once with binding buffer and treated with various concentrations of different reagents (including GDNF, PI-PLC, PI-PLC/CM, and Ret-Fc fusion protein), either alone or in combination, in binding buffer for various periods of times. Treated cells and untreated controls were
- 15 lysed in Triton X-100 lysis buffer and immunoprecipitated with the anti-Ret antibody (Santa Cruz, C-19, Cat. #SC-167) and protein-A Sepharose as described above. Immunoprecipitates were fractionated by SDS-PAGE and transferred to nitrocellulose membranes as described by Harlow and Lane (Antibodies: A Laboratory Manual. Cold Spring Harbor Laboratory: Cold Spring Harbor, New York, 1988). The
- 20 membranes were pre-blocked with 5% BSA (Sigma) and the level of tyrosine phosphorylation of the receptor was determined by blotting the membrane with an anti-phosphotyrosine monoclonal antibody 4G10 (UBI, Cat. #05-321) at room temperature for two hours. The amount of protein included in each lane was determined by stripping and re-probing the same membrane with the anti-Ret antibody. Finally, the
- 25 membrane was treated with chemiluminescence reagents (ECL, Amersham) following the manufacturer's instructions and exposed to X-ray films (Hyperfilm-ELC, Amersham).

Treatment of Cells with PI-PLC and Generation of PI-PLC Treated Conditioned Media

- 30 In order to release GPI-linked GDNFR from the cell surface, cells were washed once with washing buffer, then incubated with 1 U/mL phosphatidylinositol specific phospholipase C (PI-PLC, Boehringer Mannheim, Cat. #1143069) in binding buffer at 37°C for 45 minutes. The cells were then washed three times with washing buffer and further processed for Ret autophosphorylation assay or cross-linking. For
- 35 generation of PI-PLC treated conditioned media (PI-PLC/CM), 8×10^6 cells were removed from tissue culture dishes by treating the cells with PBS containing 2 mM of EDTA at 37°C for 5 to 10 minutes. Cells were washed once with washing buffer,

resuspended in 1 mL of binding buffer containing 1 U/mL of PI-PLC, and incubated at 37°C for 45 minutes. The cells were pelleted, and the PI-PLC/CM was collected.

Preparation of the Ret-Fc Fusion Protein

5 A cDNA encompassing the entire coding region of c-Ret was isolated from a day 17 rat placenta cDNA library using an oligonucleotide probe corresponding to the first 20 amino acids of the mouse c-Ret (Iwamoto et al., 1993; van Heyningen, 1994). The region coding for the extracellular domain of the Ret receptor (ending with the last amino acid, R636) was fused in-frame with the DNA coding for the Fc region of
10 human IgG (IgG1) and subcloned into the expression vector pDSR2 as previously described (Bartley et al., Nature. 368, 558-560, 1994). The ret-Fc/pDSRa2 plasmid was transfected into Chinese hamster ovary (CHO) cells and the recombinant Ret-Fc fusion protein was purified by affinity chromatography using a Ni⁺⁺ column (Qiagen).

15

Preparation of Embryonic Rat Spinal Cord Motor Neuron Cultures

Enriched embryonic rat spinal cord motor neuron cultures were prepared from entire spinal cords of E15 Sprague-Dawley rat fetuses 24 hours before the experiments. The spinal cords were dissected, and the meninges and dorsal root
20 ganglia (DRGs) were removed. The spinal cords were cut into smaller fragments and digested with papain in L15 medium (Papain Kit, Worthington). The motor neurons, which are larger than other types of cells included in the dissociated cell suspension, were enriched using a 6.8% Metrizamide gradient (Camu and Henderson, J Neuroscience. 44, 59-70, 1992). Enriched motor neurons residing at the interface
25 between the metrizamide cushion and the cell suspension were collected, washed, and seeded in tissue culture dishes pre-coated with poly-L-ornithine and laminin at a density of $\sim 9 \times 10^4$ cells/cm² and were cultured at 37°C.

30 Various references are cited herein, the disclosures of which are incorporated by reference in their entireties.

While the present invention has been described in terms of preferred embodiments and exemplary nucleic acid and amino acid sequences, it is understood that variations and modifications will occur to those skilled in the art. Therefore, it is
35 intended that the appended claims cover all such equivalent variations which come within the scope of the invention as claimed.

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SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: Fox, Gary M
Jing, Shuqian
Wen, Duanzhi
- (ii) TITLE OF INVENTION: GLIAL CELL LINE-DERIVED NEUROTROPHIC
FACTOR RECEPTOR
- (iii) NUMBER OF SEQUENCES: 34
- (iv) CORRESPONDENCE ADDRESS:
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 - (E) COUNTRY: US
 - (F) ZIP: 91320-1789
- (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Floppy disk
 - (B) COMPUTER: IBM PC compatible
 - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 - (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
- (vi) CURRENT APPLICATION DATA:
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- (viii) ATTORNEY/AGENT INFORMATION:
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 - (B) REGISTRATION NUMBER: 32,727
 - (C) REFERENCE/DOCKET NUMBER: A-401A

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 2568 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 540..1934

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

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CCGGCGGGCG TGGCTGCTGC CAGACCCGGA GTTTCCTCTT TCACTGGATG GAGCTGAACT	420
TTGGGCGGCC AGAGCAGCAC AGCTGTCCGG GGATCGCTGC ACGCTGAGCT CCCTCGGCAA	480
GACCCAGCGG CGGCTCGGGA TTTTTTTGGG GGGGCGGGGA CCAGCCCCGC GCCGGCACC	539
ATG TTC CTG GCG ACC CTG TAC TTC GCG CTG CCG CTC TTG GAC TTG CTC	587
Met Phe Leu Ala Thr Leu Tyr Phe Ala Leu Pro Leu Leu Asp Leu Leu	
1 5 10 15	
CTG TCG GCC GAA GTG AGC GGC GGA GAC CGC CTG GAT TGC GTG AAA GCC	635
Leu Ser Ala Glu Val Ser Gly Gly Asp Arg Leu Asp Cys Val Lys Ala	
20 25 30	
AGT GAT CAG TGC CTG AAG GAG CAG AGC TGC AGC ACC AAG TAC CGC ACG	683
Ser Asp Gln Cys Leu Lys Glu Gln Ser Cys Ser Thr Lys Tyr Arg Thr	
35 40 45	
CTA AGG CAG TGC GTG GCG GGC AAG GAG ACC AAC TTC AGC CTG GCA TCC	731
Leu Arg Gln Cys Val Ala Gly Lys Glu Thr Asn Phe Ser Leu Ala Ser	
50 55 60	
GGC CTG GAG GCC AAG GAT GAG TGC CGC AGC GCC ATG GAG GCC CTG AAG	779
Gly Leu Glu Ala Lys Asp Glu Cys Arg Ser Ala Met Glu Ala Leu Lys	
65 70 75 80	
CAG AAG TCG CTC TAC AAC TGC CGC TGC AAG CGG GGT ATG AAG AAG GAG	827
Gln Lys Ser Leu Tyr Asn Cys Arg Cys Lys Arg Gly Met Lys Lys Glu	
85 90 95	
AAG AAC TGC CTG CGC ATT TAC TGG AGC ATG TAC CAG AGC CTG CAG GGA	875
Lys Asn Cys Leu Arg Ile Tyr Trp Ser Met Tyr Gln Ser Leu Gln Gly	
100 105 110	
AAT GAT CTG CTG GAG GAT TCC CCA TAT GAA CCA GTT AAC AGC AGA TTG	923
Asn Asp Leu Leu Glu Asp Ser Pro Tyr Glu Pro Val Asn Ser Arg Leu	
115 120 125	

TCA GAT ATA TTC CGG GTG GTC CCA TTC ATA TCA GAT GTT TTT CAG CAA Ser Asp Ile Phe Arg Val Val Pro Phe Ile Ser Asp Val Phe Gln Gln 130 135 140	971
GTG GAG CAC ATT CCC AAA GGG AAC AAC TGC CTG GAT GCA GCG AAG GCC Val Glu His Ile Pro Lys Gly Asn Asn Cys Leu Asp Ala Ala Lys Ala 145 150 155 160	1019
TGC AAC CTC GAC GAC ATT TGC AAG AAG TAC AGG TCG GCG TAC ATC ACC Cys Asn Leu Asp Asp Ile Cys Lys Lys Tyr Arg Ser Ala Tyr Ile Thr 165 170 175	1067
CCG TGC ACC ACC AGC GTG TCC AAC GAT GTC TGC AAC CGC CGC AAG TGC Pro Cys Thr Thr Ser Val Ser Asn Asp Val Cys Asn Arg Arg Lys Cys 180 185 190	1115
CAC AAG GCC CTC CGG CAG TTC TTT GAC AAG GTC CCG GCC AAG CAC AGC His Lys Ala Leu Arg Gln Phe Phe Asp Lys Val Pro Ala Lys His Ser 195 200 205	1163
TAC GGA ATG CTC TTC TGC TCC TGC CGG GAC ATC GCC TGC ACA GAG CGG Tyr Gly Met Leu Phe Cys Ser Cys Arg Asp Ile Ala Cys Thr Glu Arg 210 215 220	1211
AGG CGA CAG ACC ATC GTG CCT GTG TGC TCC TAT GAA GAG AGG GAG AAG Arg Arg Gln Thr Ile Val Pro Val Cys Ser Tyr Glu Glu Arg Glu Lys 225 230 235 240	1259
CCC AAC TGT TTG AAT TTG CAG GAC TCC TGC AAG ACG AAT TAC ATC TGC Pro Asn Cys Leu Asn Leu Gln Asp Ser Cys Lys Thr Asn Tyr Ile Cys 245 250 255	1307
AGA TCT CGC CTT GCG GAT TTT TTT ACC AAC TGC CAG CCA GAG TCA AGG Arg Ser Arg Leu Ala Asp Phe Phe Thr Asn Cys Gln Pro Glu Ser Arg 260 265 270	1355
TCT GTC AGC AGC TGT CTA AAG GAA AAC TAC GCT GAC TGC CTC CTC GCC Ser Val Ser Ser Cys Leu Lys Glu Asn Tyr Ala Asp Cys Leu Leu Ala 275 280 285	1403
TAC TCG GGG CTT ATT GGC ACA GTC ATG ACC CCC AAC TAC ATA GAC TCC Tyr Ser Gly Leu Ile Gly Thr Val Met Thr Pro Asn Tyr Ile Asp Ser 290 295 300	1451
AGT AGC CTC AGT GTG GCC CCA TGG TGT GAC TGC AGC AAC AGT GGG AAC Ser Ser Leu Ser Val Ala Pro Trp Cys Asp Cys Ser Asn Ser Gly Asn 305 310 315 320	1499
GAC CTA GAA GAG TGC TTG AAA TTT TTG AAT TTC TTC AAG GAC AAT ACA Asp Leu Glu Glu Cys Leu Lys Phe Leu Asn Phe Phe Lys Asp Asn Thr 325 330 335	1547
TGT CTT AAA AAT GCA ATT CAA GCC TTT GGC AAT GGC TCC GAT GTG ACC Cys Leu Lys Asn Ala Ile Gln Ala Phe Gly Asn Gly Ser Asp Val Thr 340 345 350	1595

GTG TGG CAG CCA GCC TTC CCA GTA CAG ACC ACC ACT GCC ACT ACC ACC Val Trp Gln Pro Ala Phe Pro Val Gln Thr Thr Thr Thr Ala Thr Thr Thr 355 360 365	1643
ACT GCC CTC CGG GTT AAG AAC AAG CCC CTG GGG CCA GCA GGG TCT GAG Thr Ala Leu Arg Val Lys Asn Lys Pro Leu Gly Pro Ala Gly Ser Glu 370 375 380	1691
AAT GAA ATT CCC ACT CAT GTT TTG CCA CCG TGT GCA AAT TTA CAG GCA Asn Glu Ile Pro Thr His Val Leu Pro Pro Cys Ala Asn Leu Gln Ala 385 390 395 400	1739
CAG AAG CTG AAA TCC AAT GTG TCG GGC AAT ACA CAC CTC TGT ATT TCC Gln Lys Leu Lys Ser Asn Val Ser Gly Asn Thr His Leu Cys Ile Ser 405 410 415	1787
AAT GGT AAT TAT GAA AAA GAA GGT CTC GGT GCT TCC AGC CAC ATA ACC Asn Gly Asn Tyr Glu Lys Glu Gly Leu Gly Ala Ser Ser His Ile Thr 420 425 430	1835
ACA AAA TCA ATG GCT GCT CCT CCA AGC TGT GGT CTG AGC CCA CTG CTG Thr Lys Ser Met Ala Ala Pro Pro Ser Cys Gly Leu Ser Pro Leu Leu 435 440 445	1883
GTC CTG GTG GTA ACC GCT CTG TCC ACC CTA TTA TCT TTA ACA GAA ACA Val Leu Val Val Thr Ala Leu Ser Thr Leu Leu Ser Leu Thr Glu Thr 450 455 460	1931
TCA TAGCTGCATT AAAAAAATAC AATATGGACA TGTAAAAGA CAAAAACCAA Ser 465	1984
GTTATCTGTT TCCTGTTCTC TTGTATAGCT GAAATTCCAG TTTAGGAGCT CAGTTGAGAA	2044
ACAGTTCCAT TCAACTGGAA CATTTTTTTT TTTNCCTTTT AAGAAAGCTT CTTGTGATCC	2104
TTNGGGGCTT CTGTGAAAAA CCTGATGCAG TGCTCCATCC AAATCAGAA GGCTTTGGGA	2164
TATGCTGTAT TTAAAGGGA CAGTTTGTA CTTGGGCTGT AAAGCAAACT GGGGCTGTGT	2224
TTTCGATGAT GATGATNATC ATGATNATGA TNNNNNNNNN NNNNNNNNNN NNNNNNNNNN	2284
NNNNNNNNNN GATTTTAACA GTTTTACTTC TGGCCTTTCC TAGCTAGAGA AGGAGTTAAT	2344
ATTTCTAAGG TAACTCCCAT ATCTCCTTTA ATGACATTGA TTTCTAATGA TATAAATTC	2404
AGCCTACATT GATGCCAAGC TTTTGTGCCA CAAAGAAGAT TCTTACCAAG AGTGGGCTTT	2464
GTGGAAACAG CTGGTACTGA TGTTACCTT TATATATGTA CTAGCATTTT CCACGCTGAT	2524
GTATATGTAC TGTAACAGT TCTGCACTCT TGTACAAAAG AAAA	2568

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 465 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

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Met Phe Leu Ala Thr Leu Tyr Phe Ala Leu Pro Leu Leu Asp Leu Leu
 1             5             10             15

Leu Ser Ala Glu Val Ser Gly Gly Asp Arg Leu Asp Cys Val Lys Ala
          20             25             30

Ser Asp Gln Cys Leu Lys Glu Gln Ser Cys Ser Thr Lys Tyr Arg Thr
          35             40             45

Leu Arg Gln Cys Val Ala Gly Lys Glu Thr Asn Phe Ser Leu Ala Ser
          50             55             60

Gly Leu Glu Ala Lys Asp Glu Cys Arg Ser Ala Met Glu Ala Leu Lys
          65             70             75             80

Gln Lys Ser Leu Tyr Asn Cys Arg Cys Lys Arg Gly Met Lys Lys Glu
          85             90             95

Lys Asn Cys Leu Arg Ile Tyr Trp Ser Met Tyr Gln Ser Leu Gln Gly
          100            105            110

Asn Asp Leu Leu Glu Asp Ser Pro Tyr Glu Pro Val Asn Ser Arg Leu
          115            120            125

Ser Asp Ile Phe Arg Val Val Pro Phe Ile Ser Asp Val Phe Gln Gln
          130            135            140

Val Glu His Ile Pro Lys Gly Asn Asn Cys Leu Asp Ala Ala Lys Ala
          145            150            155            160

Cys Asn Leu Asp Asp Ile Cys Lys Lys Tyr Arg Ser Ala Tyr Ile Thr
          165            170            175

Pro Cys Thr Thr Ser Val Ser Asn Asp Val Cys Asn Arg Arg Lys Cys
          180            185            190

His Lys Ala Leu Arg Gln Phe Phe Asp Lys Val Pro Ala Lys His Ser
          195            200            205

Tyr Gly Met Leu Phe Cys Ser Cys Arg Asp Ile Ala Cys Thr Glu Arg
          210            215            220

Arg Arg Gln Thr Ile Val Pro Val Cys Ser Tyr Glu Glu Arg Glu Lys
          225            230            235            240

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Pro Asn Cys Leu Asn Leu Gln Asp Ser Cys Lys Thr Asn Tyr Ile Cys
 245 250 255
 Arg Ser Arg Leu Ala Asp Phe Phe Thr Asn Cys Gln Pro Glu Ser Arg
 260 265 270
 Ser Val Ser Ser Cys Leu Lys Glu Asn Tyr Ala Asp Cys Leu Leu Ala
 275 280 285
 Tyr Ser Gly Leu Ile Gly Thr Val Met Thr Pro Asn Tyr Ile Asp Ser
 290 295 300
 Ser Ser Leu Ser Val Ala Pro Trp Cys Asp Cys Ser Asn Ser Gly Asn
 305 310 315 320
 Asp Leu Glu Glu Cys Leu Lys Phe Leu Asn Phe Phe Lys Asp Asn Thr
 325 330 335
 Cys Leu Lys Asn Ala Ile Gln Ala Phe Gly Asn Gly Ser Asp Val Thr
 340 345 350
 Val Trp Gln Pro Ala Phe Pro Val Gln Thr Thr Thr Ala Thr Thr Thr
 355 360 365
 Thr Ala Leu Arg Val Lys Asn Lys Pro Leu Gly Pro Ala Gly Ser Glu
 370 375 380
 Asn Glu Ile Pro Thr His Val Leu Pro Pro Cys Ala Asn Leu Gln Ala
 385 390 395 400
 Gln Lys Leu Lys Ser Asn Val Ser Gly Asn Thr His Leu Cys Ile Ser
 405 410 415
 Asn Gly Asn Tyr Glu Lys Glu Gly Leu Gly Ala Ser Ser His Ile Thr
 420 425 430
 Thr Lys Ser Met Ala Ala Pro Pro Ser Cys Gly Leu Ser Pro Leu Leu
 435 440 445
 Val Leu Val Val Thr Ala Leu Ser Thr Leu Leu Ser Leu Thr Glu Thr
 450 455 460
 Ser
 465

(2) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 2138 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 302..1705

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

AGCTCGCTCT CCCGGGGCAG TGGTGTGGAT GCACCGGAGT TCGGGCGCTG GGCAAGTTGG 60
 GTCGGAAC TG AACCCCTGAA AGCGGGTCCG CCTCCCGCCC TCGCGCCCGC CCGGATCTGA 120
 GTCGCTGGCG GCGGTGGGCG GCAGAGCGAC GGGGAGTCTG CTCTCACCTT GGATGGAGCT 180
 GAACTTTGAG TGGCCAGAGG AGCGCAGTCG CCCGGGGATC GCTGCACGCT GAGCTCTCTC 240
 CCCGAGACCG GGCGGCGGCT TTGGATTTTG GGGGGGCGGG GACCAGCTGC GCGGCGGCAC 300
 C ATG TTC CTA GCC ACT CTG TAC TTC GCG CTG CCA CTC CTG GAT TTG 346
 Met Phe Leu Ala Thr Leu Tyr Phe Ala Leu Pro Leu Leu Asp Leu
 1 5 10 15
 CTG ATG TCC GCC GAG GTG AGT GGT GGA GAC CGT CTG GAC TGT GTG AAA 394
 Leu Met Ser Ala Glu Val Ser Gly Gly Asp Arg Leu Asp Cys Val Lys
 20 25 30
 GCC AGC GAT CAG TGC CTG AAG GAA CAG AGC TGC AGC ACC AAG TAC CGC 442
 Ala Ser Asp Gln Cys Leu Lys Glu Gln Ser Cys Ser Thr Lys Tyr Arg
 35 40 45
 ACA CTA AGG CAG TGC GTG GCG GGC AAG GAA ACC AAC TTC AGC CTG ACA 490
 Thr Leu Arg Gln Cys Val Ala Gly Lys Glu Thr Asn Phe Ser Leu Thr
 50 55 60
 TCC GGC CTT GAG GCC AAG GAT GAG TGC CGT AGC GCC ATG GAG GCC TTG 538
 Ser Gly Leu Glu Ala Lys Asp Glu Cys Arg Ser Ala Met Glu Ala Leu
 65 70 75
 AAG CAG AAG TCT CTG TAC AAC TGC CGC TGC AAG CGG GGC ATG AAG AAA 586
 Lys Gln Lys Ser Leu Tyr Asn Cys Arg Cys Lys Arg Gly Met Lys Lys
 80 85 90 95
 GAG AAG AAT TGT CTG CGT ATC TAC TGG AGC ATG TAC CAG AGC CTG CAG 634
 Glu Lys Asn Cys Leu Arg Ile Tyr Trp Ser Met Tyr Gln Ser Leu Gln
 100 105 110
 GGA AAT GAC CTC CTG GAA GAT TCC CCG TAT GAG CCG GTT AAC AGC AGG 682
 Gly Asn Asp Leu Leu Glu Asp Ser Pro Tyr Glu Pro Val Asn Ser Arg
 115 120 125
 TTG TCA GAT ATA TTC CGG GCA GTC CCG TTC ATA TCA GAT GTT TTC CAG 730
 Leu Ser Asp Ile Phe Arg Ala Val Pro Phe Ile Ser Asp Val Phe Gln
 130 135 140
 CAA GTG GAA CAC ATT TCC AAA GGG AAC AAC TGC CTG GAC GCA GCC AAG 778
 Gln Val Glu His Ile Ser Lys Gly Asn Asn Cys Leu Asp Ala Ala Lys
 145 150 155

GCC TGC AAC CTG GAC GAC ACC TGT AAG AAG TAC AGG TCG GCC TAC ATC Ala Cys Asn Leu Asp Asp Thr Cys Lys Lys Tyr Arg Ser Ala Tyr Ile 160 165 170 175	826
ACC CCC TGC ACC ACC AGC ATG TCC AAC GAG GTC TGC AAC CGC CGT AAG Thr Pro Cys Thr Thr Ser Met Ser Asn Glu Val Cys Asn Arg Arg Lys 180 185 190	874
TGC CAC AAG GCC CTC AGG CAG TTC TTC GAC AAG GTT CCG GCC AAG CAC Cys His Lys Ala Leu Arg Gln Phe Phe Asp Lys Val Pro Ala Lys His 195 200 205	922
AGC TAC GGG ATG CTC TTC TGC TCC TGC CGG GAC ATC GCC TGC ACC GAG Ser Tyr Gly Met Leu Phe Cys Ser Cys Arg Asp Ile Ala Cys Thr Glu 210 215 220	970
CGG CGG CGA CAG ACT ATC GTC CCC GTG TGC TCC TAT GAA GAA CGA GAG Arg Arg Arg Gln Thr Ile Val Pro Val Cys Ser Tyr Glu Glu Arg Glu 225 230 235	1018
AGG CCC AAC TGC CTG AGT CTG CAA GAC TCC TGC AAG ACC AAT TAC ATC Arg Pro Asn Cys Leu Ser Leu Gln Asp Ser Cys Lys Thr Asn Tyr Ile 240 245 250 255	1066
TGC AGA TCT CGC CTT GCA GAT TTT TTT ACC AAC TGC CAG CCA GAG TCA Cys Arg Ser Arg Leu Ala Asp Phe Phe Thr Asn Cys Gln Pro Glu Ser 260 265 270	1114
AGG TCT GTC AGC AAC TGT CTT AAG GAG AAC TAC GCA GAC TGC CTC CTG Arg Ser Val Ser Asn Cys Leu Lys Glu Asn Tyr Ala Asp Cys Leu Leu 275 280 285	1162
GCC TAC TCG GGA CTG ATT GGC ACA GTC ATG ACT CCC AAC TAC GTA GAC Ala Tyr Ser Gly Leu Ile Gly Thr Val Met Thr Pro Asn Tyr Val Asp 290 295 300	1210
TCC AGC AGC CTC AGC GTG GCA CCA TGG TGT GAC TGC AGC AAC AGC GGC Ser Ser Ser Leu Ser Val Ala Pro Trp Cys Asp Cys Ser Asn Ser Gly 305 310 315	1258
AAT GAC CTG GAA GAC TGC TTG AAA TTT CTG AAT TTT TTT AAG GAC AAT Asn Asp Leu Glu Asp Cys Leu Lys Phe Leu Asn Phe Phe Lys Asp Asn 320 325 330 335	1306
ACT TGT CTC AAA AAT GCA ATT CAA GCC TTT GGC AAT GGC TCA GAT GTG Thr Cys Leu Lys Asn Ala Ile Gln Ala Phe Gly Asn Gly Ser Asp Val 340 345 350	1354
ACC ATG TGG CAG CCA GCC CCT CCA GTC CAG ACC ACC ACT GCC ACC ACT Thr Met Trp Gln Pro Ala Pro Pro Val Gln Thr Thr Thr Ala Thr Thr 355 360 365	1402
ACC ACT GCC TTC CGG GTC AAG AAC AAG CCT CTG GGG CCA GCA GGG TCT Thr Thr Ala Phe Arg Val Lys Asn Lys Pro Leu Gly Pro Ala Gly Ser 370 375 380	1450

GAG AAT GAG ATC CCC ACA CAC GTT TTA CCA CCC TGT GCG AAT TTG CAG 1498
 Glu Asn Glu Ile Pro Thr His Val Leu Pro Pro Cys Ala Asn Leu Gln
 385 390 395

GCT CAG AAG CTG AAA TCC AAT GTG TCG GGT AGC ACA CAC CTC TGT CTT 1546
 Ala Gln Lys Leu Lys Ser Asn Val Ser Gly Ser Thr His Leu Cys Leu
 400 405 410 415

TCT GAT AGT GAT TTC GGA AAG GAT GGT CTC GCT GGT GCC TCC AGC CAC 1594
 Ser Asp Ser Asp Phe Gly Lys Asp Gly Leu Ala Gly Ala Ser Ser His
 420 425 430

ATA ACC ACA AAA TCA ATG GCT GCT CCT CCC AGC TGC AGT CTG AGC TCA 1642
 Ile Thr Thr Lys Ser Met Ala Ala Pro Pro Ser Cys Ser Leu Ser Ser
 435 440 445

CTG CCG GTG CTG ATG CTC ACC GCC CTT GCT GCC CTG TTA TCT GTA TCG 1690
 Leu Pro Val Leu Met Leu Thr Ala Leu Ala Ala Leu Leu Ser Val Ser
 450 455 460

TTG GCA GAA ACG TCG TAGCTGCATC CGGGAAAACA GTATGAAAAG ACAAAGAGA 1745
 Leu Ala Glu Thr Ser
 465

ACCAAGTATT CTGTCCCTGT CCTCTTGAT ATCTGAAAAT CCAGTTTAA AAGCTCCGTT 1805

GAGAAGCAGT TTCACCCAAC TGGAACCTTT TCCTTGTTTT TAAGAAAGCT TGTGGCCCTC 1865

AGGGGCTTCT GTTGAAGAAC TGCTACAGGG CTAATTCCAA ACCCATAAGG CTCTGGGGCG 1925

TGGTGCGGCT TAAGGGGACC ATTTGCACCA TGTAAGCAA GCTGGGCTTA TCATGTGTTT 1985

GATGGTGAGG ATGGTAGTGG TGATGATGAT GGTAATTTTA ACAGCTTGAA CCCTGTTCTC 2045

TCTACTGGTT AGGAACAGGA GATACTATTG ATAAAGATTC TTCCATGTCT TACTCAGCAG 2105

CATTGCCTTC TGAAGACAGG CCCGCAGCCG TCG 2138

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 468 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Met Phe Leu Ala Thr Leu Tyr Phe Ala Leu Pro Leu Leu Asp Leu Leu
 1 5 10 15

Met Ser Ala Glu Val Ser Gly Gly Asp Arg Leu Asp Cys Val Lys Ala
 20 25 30

Ser Asp Gln Cys Leu Lys Glu Gln Ser Cys Ser Thr Lys Tyr Arg Thr
35 40 45

Leu Arg Gln Cys Val Ala Gly Lys Glu Thr Asn Phe Ser Leu Thr Ser
50 55 60

Gly Leu Glu Ala Lys Asp Glu Cys Arg Ser Ala Met Glu Ala Leu Lys
65 70 75 80

Gln Lys Ser Leu Tyr Asn Cys Arg Cys Lys Arg Gly Met Lys Lys Glu
85 90 95

Lys Asn Cys Leu Arg Ile Tyr Trp Ser Met Tyr Gln Ser Leu Gln Gly
100 105 110

Asn Asp Leu Leu Glu Asp Ser Pro Tyr Glu Pro Val Asn Ser Arg Leu
115 120 125

Ser Asp Ile Phe Arg Ala Val Pro Phe Ile Ser Asp Val Phe Gln Gln
130 135 140

Val Glu His Ile Ser Lys Gly Asn Asn Cys Leu Asp Ala Ala Lys Ala
145 150 155 160

Cys Asn Leu Asp Asp Thr Cys Lys Lys Tyr Arg Ser Ala Tyr Ile Thr
165 170 175

Pro Cys Thr Thr Ser Met Ser Asn Glu Val Cys Asn Arg Arg Lys Cys
180 185 190

His Lys Ala Leu Arg Gln Phe Phe Asp Lys Val Pro Ala Lys His Ser
195 200 205

Tyr Gly Met Leu Phe Cys Ser Cys Arg Asp Ile Ala Cys Thr Glu Arg
210 215 220

Arg Arg Gln Thr Ile Val Pro Val Cys Ser Tyr Glu Glu Arg Glu Arg
225 230 235 240

Pro Asn Cys Leu Ser Leu Gln Asp Ser Cys Lys Thr Asn Tyr Ile Cys
245 250 255

Arg Ser Arg Leu Ala Asp Phe Phe Thr Asn Cys Gln Pro Glu Ser Arg
260 265 270

Ser Val Ser Asn Cys Leu Lys Glu Asn Tyr Ala Asp Cys Leu Leu Ala
275 280 285

Tyr Ser Gly Leu Ile Gly Thr Val Met Thr Pro Asn Tyr Val Asp Ser
290 295 300

Ser Ser Leu Ser Val Ala Pro Trp Cys Asp Cys Ser Asn Ser Gly Asn
305 310 315 320

Asp Leu Glu Asp Cys Leu Lys Phe Leu Asn Phe Phe Lys Asp Asn Thr
325 330 335

Cys Leu Lys Asn Ala Ile Gln Ala Phe Gly Asn Gly Ser Asp Val Thr
 340 345 350
 Met Trp Gln Pro Ala Pro Pro Val Gln Thr Thr Thr Ala Thr Thr Thr
 355 360 365
 Thr Ala Phe Arg Val Lys Asn Lys Pro Leu Gly Pro Ala Gly Ser Glu
 370 375 380
 Asn Glu Ile Pro Thr His Val Leu Pro Pro Cys Ala Asn Leu Gln Ala
 385 390 395 400
 Gln Lys Leu Lys Ser Asn Val Ser Gly Ser Thr His Leu Cys Leu Ser
 405 410 415
 Asp Ser Asp Phe Gly Lys Asp Gly Leu Ala Gly Ala Ser Ser His Ile
 420 425 430
 Thr Thr Lys Ser Met Ala Ala Pro Pro Ser Cys Ser Leu Ser Ser Leu
 435 440 445
 Pro Val Leu Met Leu Thr Ala Leu Ala Ala Leu Leu Ser Val Ser Leu
 450 455 460
 Ala Glu Thr Ser
 465

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3209 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 1..539
- (D) OTHER INFORMATION: /note= "1 to 539 is -237 to 301 of Figure 5 Gdnfr"

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 540..1937

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

AATCTGGCCT CGGAACACGC CATTCTCCGC GCCGCTTCCA ATAACCACTA ACATCCCTAA 60
 CGAGCATCCG AGCCGAGGGC TCTGCTCGGA AATCGTCCTG GCCCAACTCG GCCCTTCGAG 120
 CTCTCGAAGA TTACCGCATC TATTTTTTTT TTCTTTTTTT TCTTTTCCTA GCGCAGATAA 180

AGTGAGCCCG GAAAGGGAAG GAGGGGGCGG GGACACCATT GCCCTGAAAG AATAAATAAG 240
 TAAATAAACA AACTGGCTCC TCGCCGCAGC TGGACGCGGT CGGTTGAGTC CAGGTTGGGT 300
 CGGACCTGAA CCCCTAAAAG CGGAACCGCC TCCC GCCCTC GCCATCCCGG AGCTGAGTCG 360
 CCGGCGGCGG TGGCTGCTGC CAGACCCGGA GTTTCCTCTT TCACTGGATG GAGCTGAACT 420
 TTGGGCGGCC AGAGCAGCAC AGCTGTCCGG GGATCGCTGC ACGCTGAGCT CCCTCGGCAA 480
 GACCCAGCGG CGGCTCGGGA TTTTTTTGGG GGGGCGGGGA CCAGCCCCGC GCCGGCACC 539
 ATG TTC CTG GCG ACC CTG TAC TTC GCG CTG CCG CTC TTG GAC TTG CTC 587
 Met Phe Leu Ala Thr Leu Tyr Phe Ala Leu Pro Leu Leu Asp Leu Leu
 1 5 10 15
 CTG TCG GCC GAA GTG AGC GGC GGA GAC CGC CTG GAT TGC GTG AAA GCC 635
 Leu Ser Ala Glu Val Ser Gly Gly Asp Arg Leu Asp Cys Val Lys Ala
 20 25 30
 AGT GAT CAG TGC CTG AAG GAG CAG AGC TGC AGC ACC AAG TAC CGC ACG 683
 Ser Asp Gln Cys Leu Lys Glu Gln Ser Cys Ser Thr Lys Tyr Arg Thr
 35 40 45
 CTA AGG CAG TGC GTG GCG GGC AAG GAG ACC AAC TTC AGC CTG GCA TCC 731
 Leu Arg Gln Cys Val Ala Gly Lys Glu Thr Asn Phe Ser Leu Ala Ser
 50 55 60
 GGC CTG GAG GCC AAG GAT GAG TGC CGC AGC GCC ATG GAG GCC CTG AAG 779
 Gly Leu Glu Ala Lys Asp Glu Cys Arg Ser Ala Met Glu Ala Leu Lys
 65 70 75 80
 CAG AAG TCG CTC TAC AAC TGC CGC TGC AAG CGG GGT ATG AAG AAG GAG 827
 Gln Lys Ser Leu Tyr Asn Cys Arg Cys Lys Arg Gly Met Lys Lys Glu
 85 90 95
 AAG AAC TGC CTG CGC ATT TAC TGG AGC ATG TAC CAG AGC CTG CAG GGA 875
 Lys Asn Cys Leu Arg Ile Tyr Trp Ser Met Tyr Gln Ser Leu Gln Gly
 100 105 110
 AAT GAT CTG CTG GAG GAT TCC CCA TAT GAA CCA GTT AAC AGC AGA TTG 923
 Asn Asp Leu Leu Glu Asp Ser Pro Tyr Glu Pro Val Asn Ser Arg Leu
 115 120 125
 TCA GAT ATA TTC CGG GTG GTC CCA TTC ATA TCA GAT GTT TTT CAG CAA 971
 Ser Asp Ile Phe Arg Val Val Pro Phe Ile Ser Asp Val Phe Gln Gln
 130 135 140
 GTG GAG CAC ATT CCC AAA GGG AAC AAC TGC CTG GAT GCA GCG AAG GCC 1019
 Val Glu His Ile Pro Lys Gly Asn Asn Cys Leu Asp Ala Ala Lys Ala
 145 150 155 160
 TGC AAC CTC GAC GAC ATT TGC AAG AAG TAC AGG TCG GCG TAC ATC ACC 1067
 Cys Asn Leu Asp Asp Ile Cys Lys Lys Tyr Arg Ser Ala Tyr Ile Thr
 165 170 175

CCG TGC ACC ACC AGC GTG TCC AAN GAT GTC TGC AAC CGC CGC AAG TGC	1115
Pro Cys Thr Thr Ser Val Ser Xaa Asp Val Cys Asn Arg Arg Lys Cys	
180 185 190	
CAC AAG GCC CTC CGG CAG TTC TTT GAC AAG GTC CCG GCC AAG CAC AGC	1163
His Lys Ala Leu Arg Gln Phe Phe Asp Lys Val Pro Ala Lys His Ser	
195 200 205	
TAC GGA ATG CTC TTC TGC TCC TGC CGG GAC ATC GCC TGC ACA GAG CGG	1211
Tyr Gly Met Leu Phe Cys Ser Cys Arg Asp Ile Ala Cys Thr Glu Arg	
210 215 220	
AGG CGA CAG ACC ATC GTG CCT GTG TGC TCC TAT GAA GAG AGG GAG AAG	1259
Arg Arg Gln Thr Ile Val Pro Val Cys Ser Tyr Glu Glu Arg Glu Lys	
225 230 235 240	
CCC AAC TGT TTG AAT TTG CAG GAC TCC TGC AAG ACG AAT TAC ATC TGC	1307
Pro Asn Cys Leu Asn Leu Gln Asp Ser Cys Lys Thr Asn Tyr Ile Cys	
245 250 255	
AGA TCT CGC CTT GCG GAT TTT TTT ACC AAC TGC CAG CCA GAG TCA AGG	1355
Arg Ser Arg Leu Ala Asp Phe Phe Thr Asn Cys Gln Pro Glu Ser Arg	
260 265 270	
TCT GTC AGC AGC TGT CTA AAG GAA AAC TAC GCT GAC TGC CTC CTC GCC	1403
Ser Val Ser Ser Cys Leu Lys Glu Asn Tyr Ala Asp Cys Leu Leu Ala	
275 280 285	
TAC TCG GGG CTT ATT GGC ACA GTC ATG ACC CCC AAC TAC ATA GAC TCC	1451
Tyr Ser Gly Leu Ile Gly Thr Val Met Thr Pro Asn Tyr Ile Asp Ser	
290 295 300	
AGT AGC CTC AGT GTG GCC CCA TGG TGT GAC TGC AGC AAC AGT GGG AAC	1499
Ser Ser Leu Ser Val Ala Pro Trp Cys Asp Cys Ser Asn Ser Gly Asn	
305 310 315 320	
GAC CTA GAA GAG TGC TTG AAA TTT TTG AAT TTC TTC AAG GAC AAT ACA	1547
Asp Leu Glu Glu Cys Leu Lys Phe Leu Asn Phe Phe Lys Asp Asn Thr	
325 330 335	
TGT CTT AAA AAT GCA ATT CAA GCC TTT GGC AAT GGC TCC GAT GTG ACC	1595
Cys Leu Lys Asn Ala Ile Gln Ala Phe Gly Asn Gly Ser Asp Val Thr	
340 345 350	
GTG TGG CAG CCA GCC TTC CCA GTA CAG ACC ACC ACT GCC ACT ACC ACC	1643
Val Trp Gln Pro Ala Phe Pro Val Gln Thr Thr Thr Ala Thr Thr Thr	
355 360 365	
ACT GCC CTC CGG GTT AAG AAC AAG CCC CTG GGG CCA GCA GGG TCT GAG	1691
Thr Ala Leu Arg Val Lys Asn Lys Pro Leu Gly Pro Ala Gly Ser Glu	
370 375 380	
AAT GAA ATT CCC ACT CAT GTT TTG CCA CCG TGT GCA AAT TTA CAG GCA	1739
Asn Glu Ile Pro Thr His Val Leu Pro Pro Cys Ala Asn Leu Gln Ala	
385 390 395 400	

CAG AAG CTG AAA TCC AAT GTG TCG GGC AAT ACA CAC CTC TGT ATT TCC Gln Lys Leu Lys Ser Asn Val Ser Gly Asn Thr His Leu Cys Ile Ser 405 410 415	1787
AAT GGT AAT TAT GAA AAA GAA GGT CTC GGT GCT TCC AGC CAC ATA ACC Asn Gly Asn Tyr Glu Lys Glu Gly Leu Gly Ala Ser Ser His Ile Thr 420 425 430	1835
ACA AAA TCA ATG GCT GCT CCT CCA AGC TGT GGT CTG AGC CCA CTG CTG Thr Lys Ser Met Ala Ala Pro Pro Ser Cys Gly Leu Ser Pro Leu Leu 435 440 445	1883
GTC CTG GTG GTA ACC GCT CTG TCC ACC CTA TTA TCT TTA ACA GAA ACA Val Leu Val Val Thr Ala Leu Ser Thr Leu Leu Ser Leu Thr Glu Thr 450 455 460	1931
TCA TAG CTGCATTAAA AAAATACAAT ATGGACATGT AAAAAGACAA AAACCAAGTT Ser * 465	1987
ATCTGTTTCC TGTTCTCTTG TATAGCTGAA ATTCCAGTTT AGGAGCTCAG TTGAGAAACA	2047
GTTCCATTCA ACTGGAACAT TTTTTTTTTT NCCTTTTAAG AAAGCTTCTT GTGATCCTTC	2107
GGGGCTTCTG TGAAAAACCT GATGCAGTGC TCCATCCAAA CTCAGAAGGC TTTGGGATAT	2167
GCTGTATTTT AAAGGGACAG TTTGTAACCT GGGCTGTAAA GCAAACCTGGG GCTGTGTTTT	2227
CGATGATGAT GATCATCATG ATCATGATNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN	2287
NNNNNNNGAT TTTAACAGTT TTACTTCTGG CCTTTCCTAG CTAGAGAAGG AGTTAATATT	2347
TCTAAGGTAA CTCCCATATC TCCTTTAATG ACATTGATTT CTAATGATAT AAATTTTCAGC	2407
CTACATTGAT GCCAAGCTTT TTTGCCACAA AGAAGATTCT TACCAAGAGT GGGCTTTGTG	2467
GAAACAGCTG GTA CTGATGT TCACCTTTAT ATATGTACTA GCATTTTCCA CGCTGATGTT	2527
TATGTACTGT AAACAGTTCT GCACTCTTGT ACAAAGAAA AAACACCTGT CACATCCAAA	2587
TATAGTATCT GTCTTTTCGT CAAAATAGAG AGTGGGGAAT GAGTGTGCCG ATTCAATACC	2647
TCAATCCCTG AACGACACTC TCCTAATCCT AAGCCTTACC TGAGTGAGAA GCCCTTTACC	2707
TAACAAAAGT CCAATATAGC TGAAATGTCG CTCTAATACT CTTTACACAT ATGAGGTTAT	2767
ATGTAGAAAA AAATTTTACT ACTAAATGAT TTCAACTATT GGCTTTCTAT ATTTTGAAAG	2827
TAATGATATT GTCTCATTTT TTTACTGATG GTTTAATACA AAATACACAG AGCTTGTTTC	2887
CCCTCATAAG TAGTGTTTCG TCTGATATGA ACTTCACAAA TACAGCTCAT CAAAAGCAGA	2947
CTCTGAGAAG CCTCGTGCTG TAGCAGAAAAG TTCTGCATCA TGTGACTGTG GACAGGCAGG	3007
AGGAAACAGA ACAGACAAGC ATTGTCTTTT GTCATTGCTC GAAGTGCAAG CGTGCATACC	3067

TGTGGAGGGA ACTGGTGGCT GCTTGTAAT GTTCTGCAGC ATCTCTTGAC ACACTTGTC 3127
 TGACACAATC CAGTACCTTG GTTTTCAGGT TATCTGACAA AGGCAGCTTT GATTGGGACA 3187
 TGGAGGCATG GGCAGGCCGG AA 3209

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 466 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Met Phe Leu Ala Thr Leu Tyr Phe Ala Leu Pro Leu Leu Asp Leu Leu
 1 5 10 15
 Leu Ser Ala Glu Val Ser Gly Gly Asp Arg Leu Asp Cys Val Lys Ala
 20 25 30
 Ser Asp Gln Cys Leu Lys Glu Gln Ser Cys Ser Thr Lys Tyr Arg Thr
 35 40 45
 Leu Arg Gln Cys Val Ala Gly Lys Glu Thr Asn Phe Ser Leu Ala Ser
 50 55 60
 Gly Leu Glu Ala Lys Asp Glu Cys Arg Ser Ala Met Glu Ala Leu Lys
 65 70 75 80
 Gln Lys Ser Leu Tyr Asn Cys Arg Cys Lys Arg Gly Met Lys Lys Glu
 85 90 95
 Lys Asn Cys Leu Arg Ile Tyr Trp Ser Met Tyr Gln Ser Leu Gln Gly
 100 105 110
 Asn Asp Leu Leu Glu Asp Ser Pro Tyr Glu Pro Val Asn Ser Arg Leu
 115 120 125
 Ser Asp Ile Phe Arg Val Val Pro Phe Ile Ser Asp Val Phe Gln Gln
 130 135 140
 Val Glu His Ile Pro Lys Gly Asn Asn Cys Leu Asp Ala Ala Lys Ala
 145 150 155 160
 Cys Asn Leu Asp Asp Ile Cys Lys Lys Tyr Arg Ser Ala Tyr Ile Thr
 165 170 175
 Pro Cys Thr Thr Ser Val Ser Xaa Asp Val Cys Asn Arg Arg Lys Cys
 180 185 190
 His Lys Ala Leu Arg Gln Phe Phe Asp Lys Val Pro Ala Lys His Ser
 195 200 205

Tyr Gly Met Leu Phe Cys Ser Cys Arg Asp Ile Ala Cys Thr Glu Arg
210 215 220

Arg Arg Gln Thr Ile Val Pro Val Cys Ser Tyr Glu Glu Arg Glu Lys
225 230 235 240

Pro Asn Cys Leu Asn Leu Gln Asp Ser Cys Lys Thr Asn Tyr Ile Cys
245 250 255

Arg Ser Arg Leu Ala Asp Phe Phe Thr Asn Cys Gln Pro Glu Ser Arg
260 265 270

Ser Val Ser Ser Cys Leu Lys Glu Asn Tyr Ala Asp Cys Leu Leu Ala
275 280 285

Tyr Ser Gly Leu Ile Gly Thr Val Met Thr Pro Asn Tyr Ile Asp Ser
290 295 300

Ser Ser Leu Ser Val Ala Pro Trp Cys Asp Cys Ser Asn Ser Gly Asn
305 310 315 320

Asp Leu Glu Glu Cys Leu Lys Phe Leu Asn Phe Phe Lys Asp Asn Thr
325 330 335

Cys Leu Lys Asn Ala Ile Gln Ala Phe Gly Asn Gly Ser Asp Val Thr
340 345 350

Val Trp Gln Pro Ala Phe Pro Val Gln Thr Thr Thr Ala Thr Thr Thr
355 360 365

Thr Ala Leu Arg Val Lys Asn Lys Pro Leu Gly Pro Ala Gly Ser Glu
370 375 380

Asn Glu Ile Pro Thr His Val Leu Pro Pro Cys Ala Asn Leu Gln Ala
385 390 395 400

Gln Lys Leu Lys Ser Asn Val Ser Gly Asn Thr His Leu Cys Ile Ser
405 410 415

Asn Gly Asn Tyr Glu Lys Glu Gly Leu Gly Ala Ser Ser His Ile Thr
420 425 430

Thr Lys Ser Met Ala Ala Pro Pro Ser Cys Gly Leu Ser Pro Leu Leu
435 440 445

Val Leu Val Val Thr Ala Leu Ser Thr Leu Leu Ser Leu Thr Glu Thr
450 455 460

Ser *
465

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 508 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 1..508
- (D) OTHER INFORMATION: /note= "1 to 508 is -237 to 272 of Figure 5 Hsgr-21af"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

```
TCTGGCCTCG GAACACGCCA TTCTCCGCGC CGCTTCCAAT AACCACTAAC ATCCCTAACG      60
AGCATCCGAG CCGAGGGGCTC TGCTCGGAAA TCGTCCTGGC CCAACTCGGC CCTTCGAGCT      120
CTCGAAGATT ACCGCATCTA TTTTNTTTTT CTNTNTTTTC TTTTCCTAGC GCAGATAAAG      180
TGAGCCCCGA AAGGGAAGGA GGGGGCGGGG ACACCATTGC CCTGAAAGAA TAAATAAGTA      240
AATAAACAAA CTGGCTCCTC GCCGCAGCTG GACGCGGTGC GTTGAGTCCA GGTTGGGTCTG      300
GACCTGAACC CCTAAAAGCG GAACCGCCTC CCGCCCTCGC CATCCCGGAG CTGAGTCGCC      360
GGCGGCGGTG GCTGCTGCCA GACCCGGAGT TTCCTCTTTC ACTGGATGGA GCTGAACTTT      420
GGGCGGCCAG AGCAGCACAG CTGTCCGGGG ATCGCTGCAC GCTGAGCTCC CTCGGCAAGA      480
CCCAGCGGCG GCTCGGGATT TTTTGGG      508
```

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 510 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 1..510
- (D) OTHER INFORMATION: /note= "1 to 510 is -237 to 272 of Figure 5 Hsgr-21bf"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

```
AATCTGGCCT CGGAACACGC CATTCTCCGC GCCGCTTCCA ATAACCACTA ACATCCCTAA      60
```

CGAGCATCCG AGCCGAGGGC TCTGCTCGGA AATCGTCCTG GCCCAACTCG GCCCTTCGAG 120
CTCTCGAAGA TTACCGCATC TATTTTTTTT TTCTTTTTTT TCTTTTCCTA GCGCAGATAA 180
AGTGAGCCCG GAAAGGGAAG GAGGGGGCGG GGACACCATT GCCCTGAAAG AATAAATAAG 240
TAAATAAACA AACTGGCTCC TCGCCGCAGC TGGACGCGGT CGGTTGAGTC CAGGTTGGGT 300
CGGACCTGAA CCCCTAAAG CGGAACCGCC TCCCGCCCTC GCCATCCCGG AGCTGAGTCG 360
CCGGCGGCGG TGGCTGCTGC CAGACCCGGA GTTCCTCTT TCACTGGATG GAGCTGAACT 420
TTGGGCGGCC AGAGCAGCAC AGCTGTCCGG GGATCGCTGC ACGCTGAGCT CCCTCGGCAA 480
GACCCAGCGG CGGCTCGGGA TTTTTTTGGG 510

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1927 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 538..1926

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 1..537
- (D) OTHER INFORMATION: /note= "1 to 537 is -235 to 301 of Figure 5 2lacon"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

TCTGGCCTCG GAACACGCCA TTCTCCGCGC CGCTTCCAAT AACCACTAAC ATCCCTAACG 60
AGCATCCGAG CCGAGGGCTC TGCTCGGAAA TCGTCCTGGC CCAACTCGGC CCTTCGAGCT 120
CTCGAAGATT ACCGCATCTA TTTTTTTTTT CTTTTTTTTC TTTTCCTAGC GCAGATAAAG 180
TGAGCCCGGA AAGGGAAGGA GGGGGCGGGG ACACCATTGC CCTGAAAGAA TAAATAAGTA 240
AATAACA AAA CTGGCTCCTC GCCGCAGCTG GACGCGGTCG GTTGAGTCCA GGTTGGGTCTG 300
GACCTGAACC CCTAAAAGCG GAACCGCCTC CCGCCCTCGC CATCCCGGAG CTGAGTCGCC 360
GGCGGCGGTG GCTGCTGCCA GACCCGGAGT TCCTCTTTC ACTGGATGGA GCTGAACTTT 420
GGGCGGCCAG AGCAGCACAG CTGTCCGGGG ATCGCTGCAC GCTGAGCTCC CTCGGCAAGA 480
CCCAGCGGCG GCTCGGGATT TTTTGGGGG GCGGGGACC AGCCCCGCGC CGGCACC 537

ATG TTC CTG GCG NCC CTG TAC TTC GCG CTG CCG CTC TTG GAC TTG CTC	585
Met Phe Leu Ala Xaa Leu Tyr Phe Ala Leu Pro Leu Leu Asp Leu Leu	
1 5 10 15	
CTG TCG GCC GAA GTG AGC GGC GGA GAC CGC CTG GAT TGC GTG AAA GCC	633
Leu Ser Ala Glu Val Ser Gly Gly Asp Arg Leu Asp Cys Val Lys Ala	
20 25 30	
AGT GAT CAG TGC CTG AAG GAG CAG AGC TGC AGC ACC AAG TAC CGC ACG	681
Ser Asp Gln Cys Leu Lys Glu Gln Ser Cys Ser Thr Lys Tyr Arg Thr	
35 40 45	
CTA AGG CAG TGC GTG GCG GGC AAG GAG ACC AAC TTC AGC CTG GCA TCC	729
Leu Arg Gln Cys Val Ala Gly Lys Glu Thr Asn Phe Ser Leu Ala Ser	
50 55 60	
GGC CTG GAG GCC AAG GAT GAG TGC CGC AGC GCC ATG GAG GCC CTG AAG	777
Gly Leu Glu Ala Lys Asp Glu Cys Arg Ser Ala Met Glu Ala Leu Lys	
65 70 75 80	
CAG AAG TCG CTC TAC AAC TGC CGC TGC AAG CGG GGT ATG AAG AAG GAG	825
Gln Lys Ser Leu Tyr Asn Cys Arg Cys Lys Arg Gly Met Lys Lys Glu	
85 90 95	
AAG AAC TGC CTG CGC ATT TAC TGG AGC ATG TAC CAG AGC CTG CAG GGA	873
Lys Asn Cys Leu Arg Ile Tyr Trp Ser Met Tyr Gln Ser Leu Gln Gly	
100 105 110	
AAT GAT CTG CTG GAG GAT TCC CCA TAT GAA CCA GTT AAC AGC AGA TTG	921
Asn Asp Leu Leu Glu Asp Ser Pro Tyr Glu Pro Val Asn Ser Arg Leu	
115 120 125	
TCA GAT ATA TTC CGG GTG GTC CCA TTC ATA TCA GAT GTT TTT CAG CAA	969
Ser Asp Ile Phe Arg Val Val Pro Phe Ile Ser Asp Val Phe Gln Gln	
130 135 140	
GTG GAG CAC ATT CCC AAA GGG AAC AAC TGC CTG GAT GCA GCG AAG GCC	1017
Val Glu His Ile Pro Lys Gly Asn Asn Cys Leu Asp Ala Ala Lys Ala	
145 150 155 160	
TGC AAC CTC GAC GAC ATT TGC AAG AAG TAC AGG TCG GCG TAC ATC ACC	1065
Cys Asn Leu Asp Asp Ile Cys Lys Lys Tyr Arg Ser Ala Tyr Ile Thr	
165 170 175	
CCG TGC ACC ACC AGC GTG TCC AAC GAT GTC TGC AAC CGC CGC AAG TGC	1113
Pro Cys Thr Thr Ser Val Ser Asn Asp Val Cys Asn Arg Arg Lys Cys	
180 185 190	
CAC AAG GCC CTC CGG CAG TTC TTT GAC AAG GTC CCG GCC AAG CAC AGC	1161
His Lys Ala Leu Arg Gln Phe Phe Asp Lys Val Pro Ala Lys His Ser	
195 200 205	
TAC GGA ATG CTC TTC TGC TCC TGC CGG GAC ATC GCC TGC ACA GAG CGG	1209
Tyr Gly Met Leu Phe Cys Ser Cys Arg Asp Ile Ala Cys Thr Glu Arg	
210 215 220	

AGG CGA CAG ACC ATC GTG CCT GTG TGC TCC TAT GAA GAG AGG GAG AAG	1257
Arg Arg Gln Thr Ile Val Pro Val Cys Ser Tyr Glu Glu Arg Glu Lys	
225 230 235 240	
CCC AAC TGT TTG AAT TTG CAG GAC TCC TGC AAG ACG AAT TAC ATC TGC	1305
Pro Asn Cys Leu Asn Leu Gln Asp Ser Cys Lys Thr Asn Tyr Ile Cys	
245 250 255	
AGA TCT CGC CTT GCG GAT TTT TTT ACC AAC TGC CAG CCA GAG TCA AGG	1353
Arg Ser Arg Leu Ala Asp Phe Phe Thr Asn Cys Gln Pro Glu Ser Arg	
260 265 270	
TCT GTC AGC AGC TGT CTA AAG GAA AAC TAC GCT GAC TGC CTC CTC GCC	1401
Ser Val Ser Ser Cys Leu Lys Glu Asn Tyr Ala Asp Cys Leu Leu Ala	
275 280 285	
TAC TCG GGG CTT ATT GGC ACA GTC ATG ACC CCC AAC TAC ATA GAC TCC	1449
Tyr Ser Gly Leu Ile Gly Thr Val Met Thr Pro Asn Tyr Ile Asp Ser	
290 295 300	
AGT AGC CTC AGT GTG GCC CCA TGG TGT GAC TGC AGC AAC AGT GGG AAC	1497
Ser Ser Leu Ser Val Ala Pro Trp Cys Asp Cys Ser Asn Ser Gly Asn	
305 310 315 320	
GAC CTA GAA GAG TGC TTG AAA TTT TTG AAT TTC TTC AAG GAC AAT ACA	1545
Asp Leu Glu Glu Cys Leu Lys Phe Leu Asn Phe Phe Lys Asp Asn Thr	
325 330 335	
TGT CTT AAA AAT GCA ATT CAA GCC TTT GGC AAT GGC TCC GAT GTG ACC	1593
Cys Leu Lys Asn Ala Ile Gln Ala Phe Gly Asn Gly Ser Asp Val Thr	
340 345 350	
GTG TGG CAG CCA GCC TTC CCA GTA CAG ACC ACC ACT GCC ACT ACC ACC	1641
Val Trp Gln Pro Ala Phe Pro Val Gln Thr Thr Thr Ala Thr Thr Thr	
355 360 365	
ACT GCC CTC CGG GTT AAG AAC AAG CCC CTG GGG CCA GCA GGG TCT GAG	1689
Thr Ala Leu Arg Val Lys Asn Lys Pro Leu Gly Pro Ala Gly Ser Glu	
370 375 380	
AAT GAA ATT CCC ACT CAT GTT TTG CCA CCG TGT GCA AAT TTA CAG GCA	1737
Asn Glu Ile Pro Thr His Val Leu Pro Pro Cys Ala Asn Leu Gln Ala	
385 390 395 400	
CAG AAG CTG AAA TCC AAT GTG TCG GGC AAT ACA CAC CTC TGT ATT TCC	1785
Gln Lys Leu Lys Ser Asn Val Ser Gly Asn Thr His Leu Cys Ile Ser	
405 410 415	
AAT GGT AAT TAT GAA AAA GAA GGT CTC GGT GCT TCC AGC CAC ATA ACC	1833
Asn Gly Asn Tyr Glu Lys Glu Gly Leu Gly Ala Ser Ser His Ile Thr	
420 425 430	
ACA AAA TCA ATG GCT GCT CCT CCA AGC TGT GGT CTG AGC CCA CTG CTG	1881
Thr Lys Ser Met Ala Ala Pro Pro Ser Cys Gly Leu Ser Pro Leu Leu	
435 440 445	

GTC CTG GTG GTA ACC GCT CTG TCC ACC CTA TTA TCT TTA ACA GAA
 Val Leu Val Val Thr Ala Leu Ser Thr Leu Leu Ser Leu Thr Glu
 450 455 460

1926

A

1927

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 463 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

Met Phe Leu Ala Xaa Leu Tyr Phe Ala Leu Pro Leu Leu Asp Leu Leu
 1 5 10 15
 Leu Ser Ala Glu Val Ser Gly Gly Asp Arg Leu Asp Cys Val Lys Ala
 20 25 30
 Ser Asp Gln Cys Leu Lys Glu Gln Ser Cys Ser Thr Lys Tyr Arg Thr
 35 40 45
 Leu Arg Gln Cys Val Ala Gly Lys Glu Thr Asn Phe Ser Leu Ala Ser
 50 55 60
 Gly Leu Glu Ala Lys Asp Glu Cys Arg Ser Ala Met Glu Ala Leu Lys
 65 70 75 80
 Gln Lys Ser Leu Tyr Asn Cys Arg Cys Lys Arg Gly Met Lys Lys Glu
 85 90 95
 Lys Asn Cys Leu Arg Ile Tyr Trp Ser Met Tyr Gln Ser Leu Gln Gly
 100 105 110
 Asn Asp Leu Leu Glu Asp Ser Pro Tyr Glu Pro Val Asn Ser Arg Leu
 115 120 125
 Ser Asp Ile Phe Arg Val Val Pro Phe Ile Ser Asp Val Phe Gln Gln
 130 135 140
 Val Glu His Ile Pro Lys Gly Asn Asn Cys Leu Asp Ala Ala Lys Ala
 145 150 155 160
 Cys Asn Leu Asp Asp Ile Cys Lys Lys Tyr Arg Ser Ala Tyr Ile Thr
 165 170 175
 Pro Cys Thr Thr Ser Val Ser Asn Asp Val Cys Asn Arg Arg Lys Cys
 180 185 190
 His Lys Ala Leu Arg Gln Phe Phe Asp Lys Val Pro Ala Lys His Ser
 195 200 205

Tyr Gly Met Leu Phe Cys Ser Cys Arg Asp Ile Ala Cys Thr Glu Arg
 210 215 220
 Arg Arg Gln Thr Ile Val Pro Val Cys Ser Tyr Glu Glu Arg Glu Lys
 225 230 235 240
 Pro Asn Cys Leu Asn Leu Gln Asp Ser Cys Lys Thr Asn Tyr Ile Cys
 245 250 255
 Arg Ser Arg Leu Ala Asp Phe Phe Thr Asn Cys Gln Pro Glu Ser Arg
 260 265 270
 Ser Val Ser Ser Cys Leu Lys Glu Asn Tyr Ala Asp Cys Leu Leu Ala
 275 280 285
 Tyr Ser Gly Leu Ile Gly Thr Val Met Thr Pro Asn Tyr Ile Asp Ser
 290 295 300
 Ser Ser Leu Ser Val Ala Pro Trp Cys Asp Cys Ser Asn Ser Gly Asn
 305 310 315 320
 Asp Leu Glu Glu Cys Leu Lys Phe Leu Asn Phe Phe Lys Asp Asn Thr
 325 330 335
 Cys Leu Lys Asn Ala Ile Gln Ala Phe Gly Asn Gly Ser Asp Val Thr
 340 345 350
 Val Trp Gln Pro Ala Phe Pro Val Gln Thr Thr Thr Ala Thr Thr Thr
 355 360 365
 Thr Ala Leu Arg Val Lys Asn Lys Pro Leu Gly Pro Ala Gly Ser Glu
 370 375 380
 Asn Glu Ile Pro Thr His Val Leu Pro Pro Cys Ala Asn Leu Gln Ala
 385 390 395 400
 Gln Lys Leu Lys Ser Asn Val Ser Gly Asn Thr His Leu Cys Ile Ser
 405 410 415
 Asn Gly Asn Tyr Glu Lys Glu Gly Leu Gly Ala Ser Ser His Ile Thr
 420 425 430
 Thr Lys Ser Met Ala Ala Pro Pro Ser Cys Gly Leu Ser Pro Leu Leu
 435 440 445
 Val Leu Val Val Thr Ala Leu Ser Thr Leu Leu Ser Leu Thr Glu
 450 455 460

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1929 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 540..1928

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION: 1..539

(D) OTHER INFORMATION: /note= "1 to 539 is -237 to 301 of Figure 5 21bcon"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

AATCTGGCCT CGGAACACGC CATTCTCCGC GCCGCTTCCA ATAACCACTA ACATCCCTAA	60
CGAGCATCCG AGCCGAGGGC TCTGCTCGGA AATCGTCCTG GCCCAACTCG GCCCTTCGAG	120
CTCTCGAAGA TTACCGCATC TATTTTTTTT TTCTTTTTTT TCTTTTCCTA GCGCAGATAA	180
AGTGAGCCCG GAAAGGGAAG GAGGGGGCGG GGACACCATT GCCCTGAAAG AATAAATAAG	240
TAAATAAACA AACTGGCTCC TCGCCGCAGC TGGACGCGGT CGGTTGAGTC CAGGTTGGGT	300
CGGACCTGAA CCCCTAAAAG CGGAACCGCC TCCCGCCCTC GCCATCCCGG AGCTGAGTCG	360
CCGGCGGCGG TGGCTGCTGC CAGACCCGGA GTTTCCTCTT TCACTGGATG GAGCTGAACT	420
TTGGGCGGCC AGAGCAGCAC AGCTGTCCGG GGATCGCTGC ACGCTGAGCT CCCTCGGCAA	480
GACCCAGCGG CGGCTCGGA TTTTTTTGGG GGGGCGGGGA CCAGCCCCGC GCCGGCACC	539
ATG TTC CTG GCG ACC CTG TAC TTC GCG CTG CCG CTC TTG GAC TTG CTC	587
Met Phe Leu Ala Thr Leu Tyr Phe Ala Leu Pro Leu Leu Asp Leu Leu	
1 5 10 15	
CTG TCG GCC GAA GTG AGC GGC GGA GAC CGC CTG GAT TGC GTG AAA GCC	635
Leu Ser Ala Glu Val Ser Gly Gly Asp Arg Leu Asp Cys Val Lys Ala	
20 25 30	
AGT GAT CAG TGC CTG AAG GAG CAG AGC TGC AGC ACC AAG TAC CGC ACG	683
Ser Asp Gln Cys Leu Lys Glu Gln Ser Cys Ser Thr Lys Tyr Arg Thr	
35 40 45	
CTA AGG CAG TGC GTG GCG GGC AAG GAG ACC AAC TTC AGC CTG GCA TCC	731
Leu Arg Gln Cys Val Ala Gly Lys Glu Thr Asn Phe Ser Leu Ala Ser	
50 55 60	
GGC CTG GAG GCC AAG GAT GAG TGC CGC AGC GCC ATG GAG GCC CTG AAG	779
Gly Leu Glu Ala Lys Asp Glu Cys Arg Ser Ala Met Glu Ala Leu Lys	
65 70 75 80	

CAG AAG TCG CTC TAC AAC TGC CGC TGC AAG CGG GGT ATG AAG AAG GAG Gln Lys Ser Leu Tyr Asn Cys Arg Cys Lys Arg Gly Met Lys Lys Glu 85 90 95	827
AAG AAC TGC CTG CGC ATT TAC TGG AGC ATG TAC CAG AGC CTG CAG GGA Lys Asn Cys Leu Arg Ile Tyr Trp Ser Met Tyr Gln Ser Leu Gln Gly 100 105 110	875
AAT GAT CTG CTG GAG GAT TCC CCA TAT GAA CCA GTT AAC AGC AGA TTG Asn Asp Leu Leu Glu Asp Ser Pro Tyr Glu Pro Val Asn Ser Arg Leu 115 120 125	923
TCA GAT ATA TTC CGG GTG GTC CCA TTC ATA TCA GAT GTT TTT CAG CAA Ser Asp Ile Phe Arg Val Val Pro Phe Ile Ser Asp Val Phe Gln Gln 130 135 140	971
GTG GAG CAC ATT CCC AAA GGG AAC AAC TGC CTG GAT GCA GCG AAG GCC Val Glu His Ile Pro Lys Gly Asn Asn Cys Leu Asp Ala Ala Lys Ala 145 150 155 160	1019
TGC AAC CTC GAC GAC ATT TGC AAG AAG TAC AGG TCG GCG TAC ATC ACC Cys Asn Leu Asp Asp Ile Cys Lys Lys Tyr Arg Ser Ala Tyr Ile Thr 165 170 175	1067
CCG TGC ACC ACC AGC GTG TCC AAC GAT GTC TGC AAC CGC CGC AAG TGC Pro Cys Thr Thr Ser Val Ser Asn Asp Val Cys Asn Arg Arg Lys Cys 180 185 190	1115
CAC AAG GCC CTC CGG CAG TTC TTT GAC AAG GTC CCG GCC AAG CAC AGC His Lys Ala Leu Arg Gln Phe Phe Asp Lys Val Pro Ala Lys His Ser 195 200 205	1163
TAC GGA ATG CTC TTC TGC TCC TGC CGG GAC ATC GCC TGC ACA GAG CGG Tyr Gly Met Leu Phe Cys Ser Cys Arg Asp Ile Ala Cys Thr Glu Arg 210 215 220	1211
AGG CGA CAG ACC ATC GTG CCT GTG TGC TCC TAT GAA GAG AGG GAG AAG Arg Arg Gln Thr Ile Val Pro Val Cys Ser Tyr Glu Glu Arg Glu Lys 225 230 235 240	1259
CCC AAC TGT TTG AAT TTG CAG GAC TCC TGC AAG ACG AAT TAC ATC TGC Pro Asn Cys Leu Asn Leu Gln Asp Ser Cys Lys Thr Asn Tyr Ile Cys 245 250 255	1307
AGA TCT CGC CTT GCG GAT TTT TTT ACC AAC TGC CAG CCA GAG TCA AGG Arg Ser Arg Leu Ala Asp Phe Phe Thr Asn Cys Gln Pro Glu Ser Arg 260 265 270	1355
TCT GTC AGC AGC TGT CTA AAG GAA AAC TAC GCT GAC TGC CTC CTC GCC Ser Val Ser Ser Cys Leu Lys Glu Asn Tyr Ala Asp Cys Leu Leu Ala 275 280 285	1403
TAC TCG GGG CTT ATT GGC ACA GTC ATG ACC CCC AAC TAC ATA GAC TCC Tyr Ser Gly Leu Ile Gly Thr Val Met Thr Pro Asn Tyr Ile Asp Ser 290 295 300	1451

AGT AGC CTC AGT GTG GCC CCA TGG TGT GAC TGC AGC AAC AGT GGG AAC	1499
Ser Ser Leu Ser Val Ala Pro Trp Cys Asp Cys Ser Asn Ser Gly Asn	
305 310 315 320	
GAC CTA GAA GAG TGC TTG AAA TTT TTG AAT TTC TTC AAG GAC AAT ACA	1547
Asp Leu Glu Glu Cys Leu Lys Phe Leu Asn Phe Phe Lys Asp Asn Thr	
325 330 335	
TGT CTT AAA AAT GCA ATT CAA GCC TTT GGC AAT GGC TCC GAT GTG ACC	1595
Cys Leu Lys Asn Ala Ile Gln Ala Phe Gly Asn Gly Ser Asp Val Thr	
340 345 350	
GTG TGG CAG CCA GCC TTC CCA GTA CAG ACC ACC ACT GCC ACT ACC ACC	1643
Val Trp Gln Pro Ala Phe Pro Val Gln Thr Thr Thr Ala Thr Thr Thr	
355 360 365	
ACT GCC CTC CGG GTT AAG AAC AAG CCC CTG GGG CCA GCA GGG TCT GAG	1691
Thr Ala Leu Arg Val Lys Asn Lys Pro Leu Gly Pro Ala Gly Ser Glu	
370 375 380	
AAT GAA ATT CCC ACT CAT GTT TTG CCA CCG TGT GCA AAT TTA CAG GCA	1739
Asn Glu Ile Pro Thr His Val Leu Pro Pro Cys Ala Asn Leu Gln Ala	
385 390 395 400	
CAG AAG CTG AAA TCC AAT GTG TCG GGC AAT ACA CAC CTC TGT ATT TCC	1787
Gln Lys Leu Lys Ser Asn Val Ser Gly Asn Thr His Leu Cys Ile Ser	
405 410 415	
AAT GGT AAT TAT GAA AAA GAA GGT CTC GGT GCT TCC AGC CAC ATA ACC	1835
Asn Gly Asn Tyr Glu Lys Glu Gly Leu Gly Ala Ser Ser His Ile Thr	
420 425 430	
ACA AAA TCA ATG GCT GCT CCT CCA AGC TGT GGT CTG AGC CCA CTG CTG	1883
Thr Lys Ser Met Ala Ala Pro Pro Ser Cys Gly Leu Ser Pro Leu Leu	
435 440 445	
GTC CTG GTG GTA ACC GCT CTG TCC ACC CTA TTA TCT TTA ACA GAA	1928
Val Leu Val Val Thr Ala Leu Ser Thr Leu Leu Ser Leu Thr Glu	
450 455 460	
A	1929

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 463 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

Met	Phe	Leu	Ala	Thr	Leu	Tyr	Phe	Ala	Leu	Pro	Leu	Leu	Asp	Leu	Leu
1					5				10					15	

Leu Ser Ala Glu Val Ser Gly Gly Asp Arg Leu Asp Cys Val Lys Ala
20 25 30

Ser Asp Gln Cys Leu Lys Glu Gln Ser Cys Ser Thr Lys Tyr Arg Thr
35 40 45

Leu Arg Gln Cys Val Ala Gly Lys Glu Thr Asn Phe Ser Leu Ala Ser
50 55 60

Gly Leu Glu Ala Lys Asp Glu Cys Arg Ser Ala Met Glu Ala Leu Lys
65 70 75 80

Gln Lys Ser Leu Tyr Asn Cys Arg Cys Lys Arg Gly Met Lys Lys Glu
85 90 95

Lys Asn Cys Leu Arg Ile Tyr Trp Ser Met Tyr Gln Ser Leu Gln Gly
100 105 110

Asn Asp Leu Leu Glu Asp Ser Pro Tyr Glu Pro Val Asn Ser Arg Leu
115 120 125

Ser Asp Ile Phe Arg Val Val Pro Phe Ile Ser Asp Val Phe Gln Gln
130 135 140

Val Glu His Ile Pro Lys Gly Asn Asn Cys Leu Asp Ala Ala Lys Ala
145 150 155 160

Cys Asn Leu Asp Asp Ile Cys Lys Lys Tyr Arg Ser Ala Tyr Ile Thr
165 170 175

Pro Cys Thr Thr Ser Val Ser Asn Asp Val Cys Asn Arg Arg Lys Cys
180 185 190

His Lys Ala Leu Arg Gln Phe Phe Asp Lys Val Pro Ala Lys His Ser
195 200 205

Tyr Gly Met Leu Phe Cys Ser Cys Arg Asp Ile Ala Cys Thr Glu Arg
210 215 220

Arg Arg Gln Thr Ile Val Pro Val Cys Ser Tyr Glu Glu Arg Glu Lys
225 230 235 240

Pro Asn Cys Leu Asn Leu Gln Asp Ser Cys Lys Thr Asn Tyr Ile Cys
245 250 255

Arg Ser Arg Leu Ala Asp Phe Phe Thr Asn Cys Gln Pro Glu Ser Arg
260 265 270

Ser Val Ser Ser Cys Leu Lys Glu Asn Tyr Ala Asp Cys Leu Leu Ala
275 280 285

Tyr Ser Gly Leu Ile Gly Thr Val Met Thr Pro Asn Tyr Ile Asp Ser
290 295 300

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Ser Ser Leu Ser Val Ala Pro Trp Cys Asp Cys Ser Asn Ser Gly Asn
305                      310                      315                      320

Asp Leu Glu Glu Cys Leu Lys Phe Leu Asn Phe Phe Lys Asp Asn Thr
                      325                      330                      335

Cys Leu Lys Asn Ala Ile Gln Ala Phe Gly Asn Gly Ser Asp Val Thr
                      340                      345                      350

Val Trp Gln Pro Ala Phe Pro Val Gln Thr Thr Thr Ala Thr Thr Thr
                      355                      360                      365

Thr Ala Leu Arg Val Lys Asn Lys Pro Leu Gly Pro Ala Gly Ser Glu
370                      375                      380

Asn Glu Ile Pro Thr His Val Leu Pro Pro Cys Ala Asn Leu Gln Ala
385                      390                      395                      400

Gln Lys Leu Lys Ser Asn Val Ser Gly Asn Thr His Leu Cys Ile Ser
                      405                      410                      415

Asn Gly Asn Tyr Glu Lys Glu Gly Leu Gly Ala Ser Ser His Ile Thr
                      420                      425                      430

Thr Lys Ser Met Ala Ala Pro Pro Ser Cys Gly Leu Ser Pro Leu Leu
435                      440                      445

Val Leu Val Val Thr Ala Leu Ser Thr Leu Leu Ser Leu Thr Glu
450                      455                      460

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(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 699 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 1..699
- (D) OTHER INFORMATION: /note= "1 to 699 is 814 to 1512 of Figure 5 Hsgr-29a"

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 2..697

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

```

G TCG GCG TAC ATC ACC CCG TGC ACC ACC AGC GTG TCC AAT GAT GTC
Ser Ala Tyr Ile Thr Pro Cys Thr Thr Ser Val Ser Asn Asp Val
  1                      5                      10                      15

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TGC AAC CGC CGC AAG TGC CAC AAG GCC CTC CGG CAG TTC TTT GAC AAG Cys Asn Arg Arg Lys Cys His Lys Ala Leu Arg Gln Phe Phe Asp Lys	94
20 25 30	
GTC CCG GCC AAG CAC AGC TAC GGA ATG CTC TTC TGC TCC TGC CGG GAC Val Pro Ala Lys His Ser Tyr Gly Met Leu Phe Cys Ser Cys Arg Asp	142
35 40 45	
ATC GCC TGC ACA GAG CGG AGG CGA CAG ACC ATC GTG CCT GTG TGC TCC Ile Ala Cys Thr Glu Arg Arg Arg Gln Thr Ile Val Pro Val Cys Ser	190
50 55 60	
TAT GAA GAG AGG GAG AAG CCC AAC TGT TTG AAT TTG CAG GAC TCC TGC Tyr Glu Glu Arg Glu Lys Pro Asn Cys Leu Asn Leu Gln Asp Ser Cys	238
65 70 75	
AAG ACG AAT TAC ATC TGC AGA TCT CGC CTT GCG GAT TTT TTT ACC AAC Lys Thr Asn Tyr Ile Cys Arg Ser Arg Leu Ala Asp Phe Phe Thr Asn	286
80 85 90 95	
TGC CAG CCA GAG TCA AGG TCT GTC AGC AGC TGT CTA AAG GAA AAC TAC Cys Gln Pro Glu Ser Arg Ser Val Ser Ser Cys Leu Lys Glu Asn Tyr	334
100 105 110	
GCT GAC TGC CTC CTC GCC TAC TCG GGG CTT ATT GGC ACA GTC ATG ACC Ala Asp Cys Leu Leu Ala Tyr Ser Gly Leu Ile Gly Thr Val Met Thr	382
115 120 125	
CCC AAC TAC ATA GAC TCC AGT AGC CTC AGT GTG GCC CCA TGG TGT GAC Pro Asn Tyr Ile Asp Ser Ser Ser Leu Ser Val Ala Pro Trp Cys Asp	430
130 135 140	
TGC AGC AAC AGT GGG AAC GAC CTA GAA GAG TGC TTG AAA TTT TTG AAT Cys Ser Asn Ser Gly Asn Asp Leu Glu Glu Cys Leu Lys Phe Leu Asn	478
145 150 155	
TTC TTC AAG GAC AAT ACA TGT CTT AAA AAT GCA ATT CAA GCC TTT GGC Phe Phe Lys Asp Asn Thr Cys Leu Lys Asn Ala Ile Gln Ala Phe Gly	526
160 165 170 175	
AAT GGC TCC GAT GTG ACC GTG TGG CAG CCA GCC TTC CCA GTA CAG ACC Asn Gly Ser Asp Val Thr Val Trp Gln Pro Ala Phe Pro Val Gln Thr	574
180 185 190	
ACC ACT GCC GCT ACC ACC ACT GCC CTC CGG GTT AAG AAC AAG CCC CTG Thr Thr Ala Ala Thr Thr Thr Ala Leu Arg Val Lys Asn Lys Pro Leu	622
195 200 205	
GGG CCA GCA GGG TCT GAG AAT GAA ATT CCC ACT CAT GTT TTG CCA CCG Gly Pro Ala Gly Ser Glu Asn Glu Ile Pro Thr His Val Leu Pro Pro	670
210 215 220	
TGT GCA AAT TTA CAG GCA CAG AAG CTG AA Cys Ala Asn Leu Gln Ala Gln Lys Leu	699
225 230	

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 232 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

```

Ser Ala Tyr Ile Thr Pro Cys Thr Thr Ser Val Ser Asn Asp Val Cys
 1           5           10           15

Asn Arg Arg Lys Cys His Lys Ala Leu Arg Gln Phe Phe Asp Lys Val
 20           25           30

Pro Ala Lys His Ser Tyr Gly Met Leu Phe Cys Ser Cys Arg Asp Ile
 35           40           45

Ala Cys Thr Glu Arg Arg Arg Gln Thr Ile Val Pro Val Cys Ser Tyr
 50           55           60

Glu Glu Arg Glu Lys Pro Asn Cys Leu Asn Leu Gln Asp Ser Cys Lys
 65           70           75           80

Thr Asn Tyr Ile Cys Arg Ser Arg Leu Ala Asp Phe Phe Thr Asn Cys
 85           90           95

Gln Pro Glu Ser Arg Ser Val Ser Ser Cys Leu Lys Glu Asn Tyr Ala
100           105           110

Asp Cys Leu Leu Ala Tyr Ser Gly Leu Ile Gly Thr Val Met Thr Pro
115           120           125

Asn Tyr Ile Asp Ser Ser Ser Leu Ser Val Ala Pro Trp Cys Asp Cys
130           135           140

Ser Asn Ser Gly Asn Asp Leu Glu Glu Cys Leu Lys Phe Leu Asn Phe
145           150           155           160

Phe Lys Asp Asn Thr Cys Leu Lys Asn Ala Ile Gln Ala Phe Gly Asn
165           170           175

Gly Ser Asp Val Thr Val Trp Gln Pro Ala Phe Pro Val Gln Thr Thr
180           185           190

Thr Ala Ala Thr Thr Thr Ala Leu Arg Val Lys Asn Lys Pro Leu Gly
195           200           205

Pro Ala Gly Ser Glu Asn Glu Ile Pro Thr His Val Leu Pro Pro Cys
210           215           220

Ala Asn Leu Gln Ala Gln Lys Leu
225           230

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(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2157 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 2..886

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 1..2157
- (D) OTHER INFORMATION: /note= "1 to 2157 is 814 to 2971 of Figure 5 29brc"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

G TCG GCG TAC ATC ACC CCG TGC ACC ACC AGC GTG TCC AAT GAT GTC	46
Ser Ala Tyr Ile Thr Pro Cys Thr Thr Ser Val Ser Asn Asp Val	
1 5 10 15	
TGC AAC CGC CGC AAG TGC CAC AAG GCC CTC CGG CAG TTC TTT GAC AAG	94
Cys Asn Arg Arg Lys Cys His Lys Ala Leu Arg Gln Phe Phe Asp Lys	
20 25 30	
GTC CCG GCC AAG CAC AGC TAC GGA ATG CTC TTC TGC TCC TGC CGG GAC	142
Val Pro Ala Lys His Ser Tyr Gly Met Leu Phe Cys Ser Cys Arg Asp	
35 40 45	
ATC GCC TGC ACA GAG CGG AGG CGA CAG ACC ATC GTG CCT GTG TGC TCC	190
Ile Ala Cys Thr Glu Arg Arg Arg Gln Thr Ile Val Pro Val Cys Ser	
50 55 60	
TAT GAA GAG AGG GAG AAG CCC AAC TGT TTG AAT TTG CAG GAC TCC TGC	238
Tyr Glu Glu Arg Glu Lys Pro Asn Cys Leu Asn Leu Gln Asp Ser Cys	
65 70 75	
AAG ACG AAT TAC ATC TGC AGA TCT CGC CTT GCG GAT TTT TTT ACC AAC	286
Lys Thr Asn Tyr Ile Cys Arg Ser Arg Leu Ala Asp Phe Phe Thr Asn	
80 85 90 95	
TGC CAG CCA GAG TCA AGG TCT GTC AGC AGC TGT CTA AAG GAA AAC TAC	334
Cys Gln Pro Glu Ser Arg Ser Val Ser Ser Cys Leu Lys Glu Asn Tyr	
100 105 110	
GCT GAC TGC CTC CTC GCC TAC TCG GGG CTT ATT GGC ACA GTC ATG ACC	382
Ala Asp Cys Leu Leu Ala Tyr Ser Gly Leu Ile Gly Thr Val Met Thr	
115 120 125	

CCC AAC TAC ATA GAC TCC AGT AGC CTC AGT GTG GCC CCA TGG TGT GAC	430
Pro Asn Tyr Ile Asp Ser Ser Ser Leu Ser Val Ala Pro Trp Cys Asp	
130 135 140	
TGC AGC AAC AGT GGG AAC GAC CTA GAA GAG TGC TTG AAA TTT TTG AAT	478
Cys Ser Asn Ser Gly Asn Asp Leu Glu Glu Cys Leu Lys Phe Leu Asn	
145 150 155	
TTC TTC AAG GAC AAT ACA TGT CTT AAA AAT GCA ATT CAA GCC TTT GGC	526
Phe Phe Lys Asp Asn Thr Cys Leu Lys Asn Ala Ile Gln Ala Phe Gly	
160 165 170 175	
AAT GGC TCC GAT GTG ACC GTG TGG CAG CCA GCC TTC CCA GTA CAG ACC	574
Asn Gly Ser Asp Val Thr Val Trp Gln Pro Ala Phe Pro Val Gln Thr	
180 185 190	
ACC ACT GCC GCT ACC ACC ACT GCC CTC CGG GTT AAG AAC AAG CCC CTG	622
Thr Thr Ala Ala Thr Thr Thr Ala Leu Arg Val Lys Asn Lys Pro Leu	
195 200 205	
GGG CCA GCA GGG TCT GAG AAT GAA ATT CCC ACT CAT GTT TTG CCA CCG	670
Gly Pro Ala Gly Ser Glu Asn Glu Ile Pro Thr His Val Leu Pro Pro	
210 215 220	
TGT GCA AAT TTA CAG GCA CAG AAG CTG AAA TCC AAT GTG TCG GGC AAT	718
Cys Ala Asn Leu Gln Ala Gln Lys Leu Lys Ser Asn Val Ser Gly Asn	
225 230 235	
ACA CAC CTC TGT ATT TCC AAT GGT AAT TAT GAA AAA GAA GGT CTC GGT	766
Thr His Leu Cys Ile Ser Asn Gly Asn Tyr Glu Lys Glu Gly Leu Gly	
240 245 250 255	
GCT TCC AGC CAC ATA ACC ACA AAA TCA ATG GCT GCT CCT CCA AGC TGT	814
Ala Ser Ser His Ile Thr Thr Lys Ser Met Ala Ala Pro Pro Ser Cys	
260 265 270	
GGT CTG AGC CCA CTG CTG GTC CTG GTG GTA ACC GCT CTG TCC ACC CTA	862
Gly Leu Ser Pro Leu Leu Val Leu Val Val Thr Ala Leu Ser Thr Leu	
275 280 285	
TTA TCT TTA ACA GAA ACA TCA TAG CTGCATTAAA AAAATACAAT ATGGACATGT	916
Leu Ser Leu Thr Glu Thr Ser *	
290 295	
AAAAAGACAA AAACCAAGTT ATCTGTTTCC TGTTCTCTTG TATAGCTGAA ATTCCAGTTT	976
AGGAGCTCAG TTGAGAAACA GTTCCATTCA ACTGGAACAT TTTT TTTT TTTT CCTTTTAAGA	1036
AAGCTTCTTG TGATCCTTCG GGGCTTCTGT GAAAAACCTG ATGCAGTGCT CCATCCAAAC	1096
TCAGAAGGCT TTGGGATATG CTGTATTTTA AAGGGACAGT TTGTAACCTG GGCTGTAAAG	1156
CAAACTGGGG CTGTGTTTTT C GATGATGATG ATCATCATGA TCATGATNNN NNNNNNNNNN	1216
NNNNNNNNNN NNNNNNNNNN NNNNNNGATT TTAACAGTTT TACTTCTGGC CTTTCCTAGC	1276

TAGAGAAGGA GTTAATATTT CTAAGGTAAC TCCCATATCT CCTTTAATGA CATTGATTTC 1336
 TAATGATATA AATTTTCAGCC TACATTGATG CCAAGCTTTT TTGCCACAAA GAAGATTCTT 1396
 ACCAAGAGTG GGCTTTGTGG AAACAGCTGG TACTGATGTT CACCTTTATA TATGTACTAG 1456
 CATTTTCCAC GCTGATGTTT ATGTACTGTA AACAGTTCTG CACTCTTGTA CAAAAGAAAA 1516
 AACACCTGTC ACATCCAAAT ATAGTATCTG TCTTTTCGTC AAAATAGAGA GTGGGGAATG 1576
 AGTGTGCCGA TTCAATACCT CAATCCCTGA ACGACACTCT CCTAATCCTA AGCCTTACCT 1636
 GAGTGAGAAG CCCTTTACCT AACAAAAGTC CAATATAGCT GAAATGTCGC TCTAATACTC 1696
 TTTACACATA TGAGGTTATA TGTAGAAAAA AATTTTACTA CTAAATGATT TCAACTATTG 1756
 GCTTTCTATA TTTTGAAAGT AATGATATTG TCTCATTTTT TTAATGATGG TTTAATACAA 1816
 AATACACAGA GCTTGTTTCC CCTCATAAGT AGTGTTTCGCT CTGATATGAA CTTACAAAAT 1876
 ACAGCTCATC AAAAGCAGAC TCTGAGAAGC CTCGTGCTGT AGCAGAAAAGT TCTGCATCAT 1936
 GTGACTGTGG ACAGGCAGGA GGAAACAGAA CAGACAAGCA TTGTCTTTTG TCATTGCTCG 1996
 AAGTGCAAGC GTGCATACCT GTGGAGGGAA CTGGTGGCTG CTTGTAAATG TTCTGCAGCA 2056
 TCTCTTGACA CACTTGTCAT GACACAATCC AGTACCTTGG TTTTCAGGTT ATCTGACAAA 2116
 GGCAGCTTTG ATTGGGACAT GGAGGCATGG GCAGGCCGGA A 2157

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 295 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

Ser Ala Tyr Ile Thr Pro Cys Thr Thr Ser Val Ser Asn Asp Val Cys
 1 5 10 15
 Asn Arg Arg Lys Cys His Lys Ala Leu Arg Gln Phe Phe Asp Lys Val
 20 25 30
 Pro Ala Lys His Ser Tyr Gly Met Leu Phe Cys Ser Cys Arg Asp Ile
 35 40 45
 Ala Cys Thr Glu Arg Arg Arg Gln Thr Ile Val Pro Val Cys Ser Tyr
 50 55 60
 Glu Glu Arg Glu Lys Pro Asn Cys Leu Asn Leu Gln Asp Ser Cys Lys
 65 70 75 80

Thr Asn Tyr Ile Cys Arg Ser Arg Leu Ala Asp Phe Phe Thr Asn Cys
 85 90 95
 Gln Pro Glu Ser Arg Ser Val Ser Ser Cys Leu Lys Glu Asn Tyr Ala
 100 105 110
 Asp Cys Leu Leu Ala Tyr Ser Gly Leu Ile Gly Thr Val Met Thr Pro
 115 120 125
 Asn Tyr Ile Asp Ser Ser Ser Leu Ser Val Ala Pro Trp Cys Asp Cys
 130 135 140
 Ser Asn Ser Gly Asn Asp Leu Glu Glu Cys Leu Lys Phe Leu Asn Phe
 145 150 155 160
 Phe Lys Asp Asn Thr Cys Leu Lys Asn Ala Ile Gln Ala Phe Gly Asn
 165 170 175
 Gly Ser Asp Val Thr Val Trp Gln Pro Ala Phe Pro Val Gln Thr Thr
 180 185 190
 Thr Ala Ala Thr Thr Thr Ala Leu Arg Val Lys Asn Lys Pro Leu Gly
 195 200 205
 Pro Ala Gly Ser Glu Asn Glu Ile Pro Thr His Val Leu Pro Pro Cys
 210 215 220
 Ala Asn Leu Gln Ala Gln Lys Leu Lys Ser Asn Val Ser Gly Asn Thr
 225 230 235 240
 His Leu Cys Ile Ser Asn Gly Asn Tyr Glu Lys Glu Gly Leu Gly Ala
 245 250 255
 Ser Ser His Ile Thr Thr Lys Ser Met Ala Ala Pro Pro Ser Cys Gly
 260 265 270
 Leu Ser Pro Leu Leu Val Leu Val Val Thr Ala Leu Ser Thr Leu Leu
 275 280 285
 Ser Leu Thr Glu Thr Ser *
 290 295

(2) INFORMATION FOR SEQ ID NO:17:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 659 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS

(B) LOCATION: 2..658

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION: 1..659

(D) OTHER INFORMATION: /note= "1 to 659 is 1033 to 1691 of Figure 5 Hsgr-21ar"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

G AAT TTG CAG GAC TCC TGC AAG ACG AAT TAC ATC TGC AGA TCT CGC	46
Asn Leu Gln Asp Ser Cys Lys Thr Asn Tyr Ile Cys Arg Ser Arg	
1 5 10 15	
CTT GCG GAT TTT TTT ACC AAC TGC CAG CCA GAG TCA AGG TCT GTC AGC	94
Leu Ala Asp Phe Phe Thr Asn Cys Gln Pro Glu Ser Arg Ser Val Ser	
20 25 30	
AGC TGT CTA AAG GAA AAC TAC GCT GAC TGC CTC CTC GCC TAC TCG GGG	142
Ser Cys Leu Lys Glu Asn Tyr Ala Asp Cys Leu Leu Ala Tyr Ser Gly	
35 40 45	
CTT ATT GGC ACA GTC ATG ACC CCC AAC TAC ATA GAC TCC AGT AGC CTC	190
Leu Ile Gly Thr Val Met Thr Pro Asn Tyr Ile Asp Ser Ser Ser Leu	
50 55 60	
AGT GTG GCC CCA TGG TGT GAC TGC AGC AAC AGT GGG AAC GAC CTA GAA	238
Ser Val Ala Pro Trp Cys Asp Cys Ser Asn Ser Gly Asn Asp Leu Glu	
65 70 75	
GAG TGC TTG AAA TTT TTG AAT TTC TTC AAG GAC AAT ACA TGT CTT AAA	286
Glu Cys Leu Lys Phe Leu Asn Phe Phe Lys Asp Asn Thr Cys Leu Lys	
80 85 90 95	
AAT GCA ATT CAA GCC TTT GGC AAT GGC TCC GAT GTG ACC GTG TGG CAG	334
Asn Ala Ile Gln Ala Phe Gly Asn Gly Ser Asp Val Thr Val Trp Gln	
100 105 110	
CCA GCC TTC CCA GTA CAG ACC ACC ACT GCC ACT ACC ACC ACT GCC CTC	382
Pro Ala Phe Pro Val Gln Thr Thr Thr Ala Thr Thr Thr Thr Ala Leu	
115 120 125	
CGG GTT AAG AAC AAG CCC CTG GGG CCA GCA GGG TCT GAG AAT GAA ATT	430
Arg Val Lys Asn Lys Pro Leu Gly Pro Ala Gly Ser Glu Asn Glu Ile	
130 135 140	
CCC ACT CAT GTT TTG CCA CCG TGT GCA AAT TTA CAG GCA CAG AAG CTG	478
Pro Thr His Val Leu Pro Pro Cys Ala Asn Leu Gln Ala Gln Lys Leu	
145 150 155	
AAA TCC AAT GTG TCG GGC AAT ACA CAC CTC TGT ATT TCC AAT GGT AAT	526
Lys Ser Asn Val Ser Gly Asn Thr His Leu Cys Ile Ser Asn Gly Asn	
160 165 170 175	

TAT GAA AAA GAA GGT CTC GGT GCT TCC AGC CAC ATA ACC ACA AAA TCA 574
 Tyr Glu Lys Glu Gly Leu Gly Ala Ser Ser His Ile Thr Thr Lys Ser
 180 185 190

ATG GCT GCT CCT CCA AGC TGT GGT CTG AGC CCA CTG CTG GTC CTG GTG 622
 Met Ala Ala Pro Pro Ser Cys Gly Leu Ser Pro Leu Leu Val Leu Val
 195 200 205

GTA ACC GCT CTG TCC ACC CTA TTA TCT TTA ACA GAA A 659
 Val Thr Ala Leu Ser Thr Leu Leu Ser Leu Thr Glu
 210 215

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 219 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

Asn Leu Gln Asp Ser Cys Lys Thr Asn Tyr Ile Cys Arg Ser Arg Leu
 1 5 10 15

Ala Asp Phe Phe Thr Asn Cys Gln Pro Glu Ser Arg Ser Val Ser Ser
 20 25 30

Cys Leu Lys Glu Asn Tyr Ala Asp Cys Leu Leu Ala Tyr Ser Gly Leu
 35 40 45

Ile Gly Thr Val Met Thr Pro Asn Tyr Ile Asp Ser Ser Ser Leu Ser
 50 55 60

Val Ala Pro Trp Cys Asp Cys Ser Asn Ser Gly Asn Asp Leu Glu Glu
 65 70 75 80

Cys Leu Lys Phe Leu Asn Phe Phe Lys Asp Asn Thr Cys Leu Lys Asn
 85 90 95

Ala Ile Gln Ala Phe Gly Asn Gly Ser Asp Val Thr Val Trp Gln Pro
 100 105 110

Ala Phe Pro Val Gln Thr Thr Thr Ala Thr Thr Thr Thr Ala Leu Arg
 115 120 125

Val Lys Asn Lys Pro Leu Gly Pro Ala Gly Ser Glu Asn Glu Ile Pro
 130 135 140

Thr His Val Leu Pro Pro Cys Ala Asn Leu Gln Ala Gln Lys Leu Lys
 145 150 155 160

Ser Asn Val Ser Gly Asn Thr His Leu Cys Ile Ser Asn Gly Asn Tyr
 165 170 175

Glu Lys Glu Gly Leu Gly Ala Ser Ser His Ile Thr Thr Lys Ser Met
 180 185 190

Ala Ala Pro Pro Ser Cys Gly Leu Ser Pro Leu Leu Val Leu Val Val
 195 200 205

Thr Ala Leu Ser Thr Leu Leu Ser Leu Thr Glu
 210 215

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 630 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 3..629

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 1..630
- (D) OTHER INFORMATION: /note= "1 to 630 is 1062 to 1691 of Figure 5 Hsgr-21br"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

AC ATC TGC AGA TCT CGC CTT GCG GAT TTT TTT ACC AAC TGC CAG CCA	47
Ile Cys Arg Ser Arg Leu Ala Asp Phe Phe Thr Asn Cys Gln Pro	
1 5 10 15	
GAG TCA AGG TCT GTC AGC AGC TGT CTA AAG GAA AAC TAC GCT GAC TGC	95
Glu Ser Arg Ser Val Ser Ser Cys Leu Lys Glu Asn Tyr Ala Asp Cys	
20 25 30	
CTC CTC GCC TAC TCG GGG CTT ATT GGC ACA GTC ATG ACC CCC AAC TAC	143
Leu Leu Ala Tyr Ser Gly Leu Ile Gly Thr Val Met Thr Pro Asn Tyr	
35 40 45	
ATA GAC TCC AGT AGC CTC AGT GTG GCC CCA TGG TGT GAC TGC AGC AAC	191
Ile Asp Ser Ser Ser Leu Ser Val Ala Pro Trp Cys Asp Cys Ser Asn	
50 55 60	
AGT GGG AAC GAC CTA GAA GAG TGC TTG AAA TTT TTG AAT TTC TTC AAG	239
Ser Gly Asn Asp Leu Glu Glu Cys Leu Lys Phe Leu Asn Phe Phe Lys	
65 70 75	
GAC AAT ACA TGT CTT AAA AAT GCA ATT CAA GCC TTT GGC AAT GGC TCC	287
Asp Asn Thr Cys Leu Lys Asn Ala Ile Gln Ala Phe Gly Asn Gly Ser	
80 85 90 95	

GAT GTG ACC GTG TGG CAG CCA GCC TTC CCA GTA CAG ACC ACC ACT GCC	335
Asp Val Thr Val Trp Gln Pro Ala Phe Pro Val Gln Thr Thr Thr Ala	
100 105 110	
ACT ACC ACC ACT GCC CTC CGG GTT AAG AAC AAG CCC CTG GGG CCA GCA	383
Thr Thr Thr Thr Ala Leu Arg Val Lys Asn Lys Pro Leu Gly Pro Ala	
115 120 125	
GGG TCT GAG AAT GAA ATT CCC ACT CAT GTT TTG CCA CCG TGT GCA AAT	431
Gly Ser Glu Asn Glu Ile Pro Thr His Val Leu Pro Pro Cys Ala Asn	
130 135 140	
TTA CAG GCA CAG AAG CTG AAA TCC AAT GTG TCG GGC AAT ACA CAC CTC	479
Leu Gln Ala Gln Lys Leu Lys Ser Asn Val Ser Gly Asn Thr His Leu	
145 150 155	
TGT ATT TCC AAT GGT AAT TAT GAA AAA GAA GGT CTC GGT GCT TCC AGC	527
Cys Ile Ser Asn Gly Asn Tyr Glu Lys Glu Gly Leu Gly Ala Ser Ser	
160 165 170 175	
CAC ATA ACC ACA AAA TCA ATG GCT GCT CCT CCA AGC TGT GGT CTG AGC	575
His Ile Thr Thr Lys Ser Met Ala Ala Pro Pro Ser Cys Gly Leu Ser	
180 185 190	
CCA CTG CTG GTC CTG GTG GTA ACC GCT CTG TCC ACC CTA TTA TCT TTA	623
Pro Leu Leu Val Leu Val Val Thr Ala Leu Ser Thr Leu Leu Ser Leu	
195 200 205	
ACA GAA A	630
Thr Glu	

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 209 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

Ile Cys Arg Ser Arg Leu Ala Asp Phe Phe Thr Asn Cys Gln Pro Glu	
1 5 10 15	
Ser Arg Ser Val Ser Ser Cys Leu Lys Glu Asn Tyr Ala Asp Cys Leu	
20 25 30	
Leu Ala Tyr Ser Gly Leu Ile Gly Thr Val Met Thr Pro Asn Tyr Ile	
35 40 45	
Asp Ser Ser Ser Leu Ser Val Ala Pro Trp Cys Asp Cys Ser Asn Ser	
50 55 60	

Gly Asn Asp Leu Glu Glu Cys Leu Lys Phe Leu Asn Phe Phe Lys Asp
 65 70 75 80
 Asn Thr Cys Leu Lys Asn Ala Ile Gln Ala Phe Gly Asn Gly Ser Asp
 85 90 95
 Val Thr Val Trp Gln Pro Ala Phe Pro Val Gln Thr Thr Thr Ala Thr
 100 105 110
 Thr Thr Thr Ala Leu Arg Val Lys Asn Lys Pro Leu Gly Pro Ala Gly
 115 120 125
 Ser Glu Asn Glu Ile Pro Thr His Val Leu Pro Pro Cys Ala Asn Leu
 130 135 140
 Gln Ala Gln Lys Leu Lys Ser Asn Val Ser Gly Asn Thr His Leu Cys
 145 150 155 160
 Ile Ser Asn Gly Asn Tyr Glu Lys Glu Gly Leu Gly Ala Ser Ser His
 165 170 175
 Ile Thr Thr Lys Ser Met Ala Ala Pro Pro Ser Cys Gly Leu Ser Pro
 180 185 190
 Leu Leu Val Leu Val Val Thr Ala Leu Ser Thr Leu Leu Ser Leu Thr
 195 200 205
 Glu

(2) INFORMATION FOR SEQ ID NO:21:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1075 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 2..445

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 1..1075
- (D) OTHER INFORMATION: /note= "1 to 1075 is 1255 to 2330
of Figure 5 Hsgr-2"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

T GGG AAC GAC CTA GAA GAG TGC TTG AAA TTT TTG AAT TTC TTC AAG	46
Gly Asn Asp Leu Glu Glu Cys Leu Lys Phe Leu Asn Phe Phe Lys	
1 5 10 15	
GAC AAT ACA TGT CTT AAA AAT GCA ATT CAA GCC TTT GGC AAT GGC TCC	94
Asp Asn Thr Cys Leu Lys Asn Ala Ile Gln Ala Phe Gly Asn Gly Ser	
20 25 30	
GAT GTG ACC GTG TGG CAG CCA GCC TTC CCA GTA CAG ACC ACC ACT GCC	142
Asp Val Thr Val Trp Gln Pro Ala Phe Pro Val Gln Thr Thr Thr Ala	
35 40 45	
ACT ACC ACC ACT GCC CTC CGG GTT AAG AAC AAG CCC CTG GGC CCA GCA	190
Thr Thr Thr Thr Ala Leu Arg Val Lys Asn Lys Pro Leu Gly Pro Ala	
50 55 60	
GGG TCT GAG AAT GAA ATT CCC ACT CAT GTT TTG CCA CCG TGT GCA AAT	238
Gly Ser Glu Asn Glu Ile Pro Thr His Val Leu Pro Pro Cys Ala Asn	
65 70 75	
TTA CAG GCA CAG AAG CTG AAA TCC AAT GTG TCG GGC AAT ACA CAC CTC	286
Leu Gln Ala Gln Lys Leu Lys Ser Asn Val Ser Gly Asn Thr His Leu	
80 85 90 95	
TGT ATT TCC AAT GGT AAT TAT GAA AAA GAA GGT CTC GGT GCT TCC AGC	334
Cys Ile Ser Asn Gly Asn Tyr Glu Lys Glu Gly Leu Gly Ala Ser Ser	
100 105 110	
CAC ATA ACC ACA AAA TCA ATG GCT GCT CCT CCA AGC TGT GGT CTG AGC	382
His Ile Thr Thr Lys Ser Met Ala Ala Pro Pro Ser Cys Gly Leu Ser	
115 120 125	
CCA CTG CTG GTC CTG GTG GTA ACC GCT CTG TCC ACC CTA TTA TCT TTA	430
Pro Leu Leu Val Leu Val Val Thr Ala Leu Ser Thr Leu Leu Ser Leu	
130 135 140	
ACA GAA ACA TCA TAG CTGCATTAAA AAAATACAAT ATGGACATGT AAAAAGACAA	485
Thr Glu Thr Ser *	
145	
AAACCAAGTT ATCTGTTTCC TGTTCCTCTG TATAGCTGAA ATTCCAGTTT AGGAGCTCAG	545
TTGAGAAACA GTTCCATTCA ACTGGAACAT TTTTTTTTTT CCTTTTAAGA AAGCTTCTTG	605
TGATCCTTCG GGGCTTCTGT GAAAAACCTG ATGCAGTGCT CCATCCAAAC TCAGAAGGCT	665
TTGGGATATG CTGTATTTTA AAGGGACAGT TTGTAAGTTG GGCTGTAAAG CAACTGGGG	725
CTGTGTTTTC GATGATGATG ATCATCATGA TCATGATNNN NNNNNNNNNN NNNNNNNNNN	785
NNNNNNNNNN NNNNNNGATT TTAACAGTTT TACTTCTGGC CTTTCCTAGC TAGAGAAGGA	845
GTTAATATTT CTAAGGTAAC TCCCATATCT CCTTTAATGA CATTGATTTC TAATGATATA	905

AATTTTCAGCC TACATTGATG CCAAGCTTTT TTGCCACAAA GAAGATTCTT ACCAAGAGTG 965
 GGCTTTGTGG AACAGCTGG TACTGATGTT CACCTTTATA TATGTACTAG CATTTTCCAC 1025
 GCTGATGTTT ATGTACTGTA AACAGTTCTG CACTCTTGTA CAAAAGAAAA 1075

(2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 148 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

Gly Asn Asp Leu Glu Glu Cys Leu Lys Phe Leu Asn Phe Phe Lys Asp
 1 5 10 15
 Asn Thr Cys Leu Lys Asn Ala Ile Gln Ala Phe Gly Asn Gly Ser Asp
 20 25 30
 Val Thr Val Trp Gln Pro Ala Phe Pro Val Gln Thr Thr Thr Ala Thr
 35 40 45
 Thr Thr Thr Ala Leu Arg Val Lys Asn Lys Pro Leu Gly Pro Ala Gly
 50 55 60
 Ser Glu Asn Glu Ile Pro Thr His Val Leu Pro Pro Cys Ala Asn Leu
 65 70 75 80
 Gln Ala Gln Lys Leu Lys Ser Asn Val Ser Gly Asn Thr His Leu Cys
 85 90 95
 Ile Ser Asn Gly Asn Tyr Glu Lys Glu Gly Leu Gly Ala Ser Ser His
 100 105 110
 Ile Thr Thr Lys Ser Met Ala Ala Pro Pro Ser Cys Gly Leu Ser Pro
 115 120 125
 Leu Leu Val Leu Val Val Thr Ala Leu Ser Thr Leu Leu Ser Leu Thr
 130 135 140
 Glu Thr Ser *
 145

(2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1059 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 3..428

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION: 1..1059

(D) OTHER INFORMATION: /note= "1 to 1059 is 1272 to 2330
of Figure 5 Hsgr-9"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

AG TGC TTG AAA TTT TTG AAT TTC TTC AAG GAC AAT ACA TGT CTT AAA	47
Cys Leu Lys Phe Leu Asn Phe Phe Lys Asp Asn Thr Cys Leu Lys	
1 5 10 15	
AAT GCA ATT CAA GCC TTT GGC AAT GGC TCC GAT GTG ACC GTG TGG CAG	95
Asn Ala Ile Gln Ala Phe Gly Asn Gly Ser Asp Val Thr Val Trp Gln	
20 25 30	
CCA GCC TTC CCA GTA CAG ACC ACC ACT GCC ACT ACC ACC ACT GCC CTC	143
Pro Ala Phe Pro Val Gln Thr Thr Thr Ala Thr Thr Thr Thr Ala Leu	
35 40 45	
CGG GTT AAG AAC AAG CCC CTG GGG CCA GCA GGG TCT GAG AAT GAA ATT	191
Arg Val Lys Asn Lys Pro Leu Gly Pro Ala Gly Ser Glu Asn Glu Ile	
50 55 60	
CCC ACT CAT GTT TTG CCA CCG TGT GCA AAT TTA CAG GCA CAG AAG CTG	239
Pro Thr His Val Leu Pro Pro Cys Ala Asn Leu Gln Ala Gln Lys Leu	
65 70 75	
AAA TCC AAT GTG TCG GGC AAT ACA CAC CTC TGT ATT TCC AAT GGT AAT	287
Lys Ser Asn Val Ser Gly Asn Thr His Leu Cys Ile Ser Asn Gly Asn	
80 85 90 95	
TAT GAA AAA GAA GGT CTC GGT GCT TCC AGC CAC ATA ACC ACA AAA TCA	335
Tyr Glu Lys Glu Gly Leu Gly Ala Ser Ser His Ile Thr Thr Lys Ser	
100 105 110	
ATG GCT GCT CCT CCA AGC TGT GGT CTG AGC CCA CTG CTG GTC CTG GTG	383
Met Ala Ala Pro Pro Ser Cys Gly Leu Ser Pro Leu Leu Val Leu Val	
115 120 125	
GTA ACC GCT CTG TCC ACC CTA TTA TCT TTA ACA GAA ACA TCA TAG	428
Val Thr Ala Leu Ser Thr Leu Leu Ser Leu Thr Glu Thr Ser *	
130 135 140	
CTGCATTAAA AAAATACAAT ATGGACATGT AAAAAGACAA AAACCAAGTT ATCTGTTTCC	488
TGTTCTCTTG TATAGCTGAA ATTCCAGTTT AGGAGCTCAG TTGAGAAACA GTTCCATTCA	548
ACTGGAACAT TTTTTTTTTT TCCTTTTAAG AAAGCTTCTT GTGATCCTTT GGGGCTTCTG	608

TGAAAAACCT GATGCAGTGC TCCATCCAAA CTCAGAAGGC TTTGGGATAT GCTGTATTTT 668
 AAAGGGACAG TTTGTAACCT GGGCTGTAAA GCAAAGTGGG GCTGTGTTTT CGATGATGAT 728
 GATGATCATG ATGATGATCA TCATGATCAT GATGATGATC ATCATGATCA TGATGATGAT 788
 TTTAACAGTT TTAATTCTGG CCTTTCCTAG CTAGAGAAGG AGTTAATATT TCTAAGGTAA 848
 CTCCCATATC TCCTTTAATG ACATTGATTT CTAATGATAT AAATTCAGC CTACATTGAT 908
 GCCAAGCTTT TTTGCCACAA AGAAGATTCT TACCAAGAGT GGGCTTTGTG GAAACAGCTG 968
 GTACTGATGT TCACCTTTAT ATATGTACTA GCATTTTCCA CGCTGATGTT TATGTACTGT 1028
 AAACAGTTCT GCACTCTTGT ACAAAGAAA A 1059

(2) INFORMATION FOR SEQ ID NO:24:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 142 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

Cys Leu Lys Phe Leu Asn Phe Phe Lys Asp Asn Thr Cys Leu Lys Asn
 1 5 10 15
 Ala Ile Gln Ala Phe Gly Asn Gly Ser Asp Val Thr Val Trp Gln Pro
 20 25 30
 Ala Phe Pro Val Gln Thr Thr Thr Ala Thr Thr Thr Thr Ala Leu Arg
 35 40 45
 Val Lys Asn Lys Pro Leu Gly Pro Ala Gly Ser Glu Asn Glu Ile Pro
 50 55 60
 Thr His Val Leu Pro Pro Cys Ala Asn Leu Gln Ala Gln Lys Leu Lys
 65 70 75 80
 Ser Asn Val Ser Gly Asn Thr His Leu Cys Ile Ser Asn Gly Asn Tyr
 85 90 95
 Glu Lys Glu Gly Leu Gly Ala Ser Ser His Ile Thr Thr Lys Ser Met
 100 105 110
 Ala Ala Pro Pro Ser Cys Gly Leu Ser Pro Leu Leu Val Leu Val Val
 115 120 125
 Thr Ala Leu Ser Thr Leu Leu Ser Leu Thr Glu Thr Ser *
 130 135 140

(2) INFORMATION FOR SEQ ID NO:25:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: peptide

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

Gln	Ser	Cys	Ser	Thr	Lys	Tyr	Arg	Thr	Leu
1				5					10

(2) INFORMATION FOR SEQ ID NO:26:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: peptide

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

Cys	Lys	Arg	Gly	Met	Lys	Lys	Glu	Lys	Asn
1				5					10

(2) INFORMATION FOR SEQ ID NO:27:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: peptide

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

Leu	Leu	Glu	Asp	Ser	Pro	Tyr	Glu	Pro	Val
1				5					10

(2) INFORMATION FOR SEQ ID NO:28:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

Cys Ser Tyr Glu Glu Arg Glu Arg Pro Asn
1 5 10

(2) INFORMATION FOR SEQ ID NO:29:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 14 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

Pro Ala Pro Pro Val Gln Thr Thr Thr Ala Thr Thr Thr Thr
1 5 10

(2) INFORMATION FOR SEQ ID NO:30:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

CTGTTTGAAT TTGCAGGACT C

21

(2) INFORMATION FOR SEQ ID NO:31:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 36 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

CTCCTCTCTA AGCTTCTAAC CACAGCTTGG AGGAGC

36

(2) INFORMATION FOR SEQ ID NO:32:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 37 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

CTCCTCTCTA AGCTTCTATG GGCTCAGACC ACAGCTT

37

(2) INFORMATION FOR SEQ ID NO:33:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 60 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

CTCCTCTCTA AGCTTCTACT TGTCATCGTC GTCCTTGTAG TCACCACAGC TTGGAGGAGC

60

(2) INFORMATION FOR SEQ ID NO:34:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 60 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

CTCCTCTCTA AGCTTCTACT TGTCATCGTC GTCCTTGTAG TCTGGCTCAG ACCACAGCTT

60

CLAIMS

What is claimed is:

- 5 1. An isolated and purified protein comprising an amino acid sequence as depicted in Figure 2 or 4 (SEQ ID NO: 2 or 4) and analogs thereof wherein the protein is capable of complexing with glial cell line-derived neurotrophic factor (GDNF) and thereby mediating cell response to GDNF.
- 10 2. A protein of Claim 1 comprising the amino acid sequence as depicted in Figure 2 (SEQ ID NO: 2).
3. A protein of Claim 1 comprising the amino acid sequence as depicted in Figure 4 (SEQ ID NO:4).
- 15 4. A protein of Claim 1 comprising the amino acid sequence Ser¹⁸ through Pro⁴⁴⁶ as depicted in Figure 2 (SEQ ID NO:2).
5. A protein of Claim 1 comprising the amino acid sequence Asp²⁵ through
20 Leu⁴⁴⁷ as depicted in Figure 2 (SEQ ID NO:2).
6. A protein of Claim 1 comprising the amino acid sequence Cys²⁹ through Cys⁴⁴² as depicted in Figure 2 (SEQ ID NO:2).
- 25 7. A protein of Claim 1 comprising the amino acid sequence Ala¹⁹ through Val⁴⁵⁰ as depicted in Figure 4 (SEQ ID NO:4).
8. A protein of Claim 1 comprising the amino acid sequence Cys²⁹ through Cys⁴⁴³ as depicted in Figure 4 (SEQ ID NO:4).
- 30 9. A protein of Claim 1 which is glycosylated.
10. A protein of Claim 1 which is non-glycosylated.
- 35 11. A protein of Claims 1 to 10 which is produced by recombinant technology or chemical synthesis.

12. A pharmaceutical composition comprising a protein as claimed in any one of claims 1 to 10 in combination with a pharmaceutically acceptable carrier.

13. An isolated nucleic acid sequence encoding a neurotrophic factor receptor protein comprising an amino acid sequence as claimed in any one of claims 1 to 8.

14. An isolated nucleic acid sequence encoding a neurotrophic factor receptor protein comprising an amino acid sequence as depicted in Figure 2 or 4 (SEQ ID NO: 2 or 4) and analogs thereof wherein the protein is capable of complexing with glial cell line-derived neurotrophic factor (GDNF) and thereby mediating cell response to GDNF.

15. A nucleic acid sequence of Claim 14 encoding a neurotrophic factor receptor protein comprising the amino acid sequence as depicted in Figure 2 (SEQ ID NO: 2).

16. A nucleic acid sequence of Claim 14 encoding a neurotrophic factor receptor protein comprising the amino acid sequence as depicted in Figure 4 (SEQ ID NO:4).

17. An isolated nucleic acid sequence comprising:

- (a) a sequence set forth in Figure 1 (SEQ ID NO: 1) comprising nucleotides encoding Met¹ through Ser⁴⁶⁵ or Figure 3 (SEQ ID NO: 3) comprising nucleotides encoding Met¹ through Ser⁴⁶⁸, wherein said sequence encodes a neurotrophic factor receptor protein (GDNFR) capable of complexing with glial cell line-derived neurotrophic factor (GDNF) and thereby mediating cell response to GDNF;
- (b) a nucleic acid sequence which (1) hybridizes to a complementary sequence of (a) and (2) encodes an amino acid sequence with GDNFR activity; and
- (c) a nucleic acid sequence which but for the degeneracy of the genetic code would hybridize to a complementary sequence of (a) and (2) encodes an amino acid sequence with GDNFR activity.

18. A vector comprising a nucleic acid sequence according to any of claims 14 to 17 operatively linked to one or more operational elements capable of effecting the amplification or expression of said nucleic acid sequence.

19. A vector comprising a nucleic acid sequence encoding a neurotrophic factor receptor protein comprising the amino acid sequence as depicted in Figure 2 or 4

(SEQ ID NO: 2 or 4) operatively linked to one or more operational elements capable of effecting the amplification or expression of said nucleic acid sequence.

20. A host cell transformed or transfected with the vector of claim 18.
- 5 21. A host cell transformed or transfected with the vector of claim 19.
22. A host cell of claim 20 selected from the group consisting of mammalian cells and bacterial cells.
- 10 23. A host cell of claim 22 which is a COS-7 cell or E. coli.
24. A host cell of Claim 20 wherein said cell is suitable for human implantation and wherein said cell expresses and secretes said neurotrophic factor receptor.
- 15 25. A host cell of Claim 21 wherein said cell is suitable for human implantation and wherein said cell expresses and secretes said neurotrophic factor receptor.
26. A host cell of Claim 20 wherein said cell is transformed or transfected ex vivo.
- 20 27. A host cell of Claim 20 wherein said cell is enclosed in a semipermeable membrane suitable for human implantation.
28. A method for the production of a neurotrophic factor receptor protein comprising the steps of:
- 25 (a) culturing a host cell, containing a nucleic acid sequence encoding a neurotrophic factor receptor protein comprising an amino acid sequence as depicted in Figure 2 or 4 (SEQ ID NO: 2 or 4) and analogs thereof wherein the protein is capable of complexing with glial cell line-derived neurotrophic factor (GDNF) and thereby mediating cell response to GDNF, under conditions
- 30 suitable for the expression of said neurotrophic factor receptor protein by said host cell; and
- (b) optionally, isolating said neurotrophic factor receptor protein expressed by said host cell.
- 35 29. A method of claim 28, wherein said nucleic acid sequence encodes a neurotrophic factor receptor protein comprising the amino acid sequence as depicted in

Figure 2 (SEQ ID NO:2).

30. A method of claim 28, wherein said nucleic acid sequence encodes a neurotrophic factor receptor protein comprising the amino acid sequence as depicted in
5 Figure 4 (SEQ ID NO:4).

31. A method for the production of a neurotrophic factor receptor protein comprising the steps of:

- 10 (a) culturing a host cell transformed or transfected with a nucleic acid sequence according to claim 17 under conditions suitable for the expression of said neurotrophic factor receptor protein by said host cell; and
(b) optionally, isolating said neurotrophic factor receptor protein expressed by said host cell.

15 32. A method of claim 28 or 31, further comprising the step of refolding the isolated neurotrophic factor receptor.

33. A method of claim 28 or 31, wherein said host cell is a prokaryotic cell.

20 34. A method of claim 28 or 31, wherein said host cell is a eukaryotic cell.

35. A substantially purified neurotrophic factor receptor protein prepared according to the method of any of claims 28 to 31.

25 36. The use of the neurotrophic factor receptor protein of claim 1 for the manufacture of a pharmaceutical composition.

37. A method of treating improperly functioning dopaminergic nerve cells by administering a neurotrophic factor receptor protein of claim 1.

30 38. A method of treating Parkinson's disease by administering a neurotrophic factor receptor protein of claim 1.

39. A method of treating Alzheimer's disease by administering a neurotrophic
35 factor receptor protein of claim 1.

40. A method of treating amyotrophic lateral sclerosis by administering a

neurotrophic protein of claim 1.

41. An antibody that binds to a neurotrophic factor receptor protein comprising an amino acid sequence of SEQ ID NO:2 or SEQ ID NO:4.

5

42. The antibody of claim 41 wherein said antibody is a monoclonal antibody.

43. The antibody of claim 41 wherein said antibody is a polyclonal antibody.

10 44. An antibody produced by immunizing an animal with a neurotrophic factor receptor protein comprising an amino acid sequence of SEQ ID NO:2 or SEQ ID NO:4.

15 45. A hybridoma that produces a monoclonal antibody that binds to a neurotrophic factor receptor protein comprising an amino acid sequence of SEQ ID NO:2 or SEQ ID NO:4.

46. A device for treating nerve damage, comprising:

- 20 (a) a semipermeable membrane suitable for implantation; and
(b) cells encapsulated within said membrane, wherein said cells secrete a neurotrophic factor receptor protein according to claim 1;
said membrane being permeable to the neurotrophic factor receptor protein and impermeable to materials detrimental to said cells.

25 47. The device of claim 46, wherein said cells are naturally occurring cells that secrete said neurotrophic factor receptor protein.

48. The device of claim 46, wherein said cells have been modified to secrete said neurotrophic factor receptor protein by means of a nucleic acid sequence comprising:

- 30 (a) a sequence set forth in Figure 1 (SEQ ID NO.: 1) comprising nucleotides encoding Met¹ through Ser⁴⁶⁵ or Figure 3 (SEQ ID NO: 3) comprising nucleotides encoding Met¹ through Ser⁴⁶⁸ encoding a neurotrophic factor receptor protein (GDNFR) capable of complexing with glial cell line-derived neurotrophic factor (GDNF) and mediating cell response to GDNF;
35 (b) a nucleic acid sequence which (1) hybridizes to a complementary sequence of (a) and (2) encodes an amino acid sequence with GDNFR activity; and
(c) a nucleic acid sequence which but for the degeneracy of the genetic code would

hybridize to a complementary sequence of (a) and (2) encodes an amino acid sequence with GDNFR activity.

49. An assay device for analyzing a test sample for the presence of glial cell line-derived neurotrophic factor, comprising: a solid phase containing or coated with a GDNFR protein, wherein said GDNFR protein reacts with GDNF present in the test sample and produces a detectable reaction product indicative of the presence of GDNF.

50. A method for analyzing a test sample for the presence of glial cell line-derived neurotrophic factor, comprising: contacting the sample to an assay reagent comprising GDNFR protein, wherein said GDNFR protein reacts with GDNF present in the test sample and produces a detectable reaction product indicative of the presence of GDNF.

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FIG.1

10 30 50
AATCTGGCCTCGGAACACGCCATTCTCCGCGCCGCTTCCAATAACCACTAACATCCCTA

70 90 110
ACGAGCATCCGAGCCGAGGGCTCTGCTCGGAAATCGTCCTGGCCCAACTCGGCCCTTCGA

130 150 170
GCTCTCGAAGATTACCGCATCTATTTTTTTTTTCTTTTTTTCTTTTCCTAGCGCAGATA

190 210 230
AAGTGAGCCCGGAAAGGGAAGGAGGGGGCGGGGACACCATTGCCCTGAAAGAATAAATAA

250 270 290
GTAAATAAACAACTGGCTCCTCGCCGCAGCTGGACGCGGTCGGTTGAGTCCAGGTTGGG

310 330 350
TCGGACCTGAACCCCTAAAAGCGGAACCGCCTCCCGCCCTCGCCATCCCGGAGCTGAGTC

370 390 410
GCCGGCGGCGGTGGCTGCTGCCAGACCCGGAGTTTCCTCTTTCACTGGATGGAGCTGAAC

430 450 470
TTTGGGCGGCCAGAGCAGCACAGCTGTCCGGGGATCGCTGCACGCTGAGCTCCCTCGGCA

490 510 530
AGACCCAGCGGCGGCTCGGGATTTTTTTGGGGGGGCGGGGACCAGCCCCGCGCCGGCACC

550 570 590
ATGTTCTCTGGCGACCCTGTACTTCGCGCTGCCGCTCTTGGA CTGCTCCTGTGGCCGAA

M F L A T L Y F A L P L L D L L L S A E

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FIG.1A

610 630 650
GTGAGCGGCGAGACCGCCTGGATTGCGTGAAGCCAGTGATCAGTGCCTGAAGGAGCAG
V S G G D R L D C V K A S D Q C L K E Q

670 690 710
AGCTGCAGCACCAAGTACCGCACGCTAAGGCAGTGCGTGGCGGCAAGGAGACCAACTTC
S C S T K Y R T L R Q C V A G K E T N F

730 750 770
AGCCTGGCATCCGGCCTGGAGGCCAAGGATGAGTGCCGCAGCGCCATGGAGGCCCTGAAG
S L A S G L E A K D E C R S A M E A L K

790 810 830
CAGAAGTCGCTCTACAAC TGCCGCTGCAAGCGGGGTATGAAGAAGGAGAAGAACTGCCTG
Q K S L Y N C R C K R G M K K E K N C L

850 870 890
CGCATTTACTGGAGCATGTACCAGAGCCTGCAGGGAATGATCTGTGAGGATTCCCCA
R I Y W S M Y Q S L Q G N D L L E D S P

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FIG. 1B

910	930	950
TATGAACCAAGTTAACAGCAGATTGTCAGATATATTCCGGGTGGTCCCATTTCATATCAGAT		
Y E P V N S R L S D I F R V V P F I S D		
970	990	1010
GTTTTTCAGCAAGTGGAGCACATTCCCAAGGGAACAACCTGCCTGGATGCAGCGAAGGCC		
V F Q Q V E H I P K G N N C L D A A K A		
1030	1050	1070
TGCAACCTCGACGACATTGCAAGAAGTACAGGTGCGGTGATCACCCTCGTGCAACCA		
C N L D D I C K K Y R S A Y I T P C T T		
1090	1110	1130
AGCGTGTCCAACGATGTCTGCAACCGCGCGAAGTGCCACAAGGCCCTCCGGCAGTCTTT		
S V S N D V C N R R K C H K A L R Q F F		

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FIG.1C

1150 1170 1190
GACAAGGTCCCGGCCAAGCACAGCTACGGAATGCTCTTCTGCTCCTGCCGGGACATCGCC
D K V P A K H S Y G M L F C S C R D I A

1210 1230 1250
TGCACAGAGCGGAGCGGACAGACCATCGTGCCTGTGTCTCCTATGAAGAGAGGGAGAAG
C T E R R R Q T I V P V C S Y E E R E K

1270 1290 1310
CCCAACTGTTGAATTTGCAGGACTCCTGCAAGACGAATTACATCTGCAGATCTCGCCTT
P N C L N L Q D S C K T N Y I C R S R L

1330 1350 1370
GCGGATTTTTTACCAACTGCCAGCCAGAGTCAAGGTCTGTCAGCAGCTGTCTAAGGAA
A D F F T N C Q P E S R S V S S C L K E

1390 1410 1430
AACTACGCTGACTGCCCTCGCCTACTCGGGGCTTATTGGCACAGTCATGACCCCAAC
N Y A D C L L A Y S G L I G T V M T P N

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FIG.1D

1450	1470	1490
TACATAGACTCCAGTAGCCTCAGTGTGGCCCCATGGTGTGACTGCAGCAACAGTGGGAAC		
Y I D S S S L S V A P W C D C S N S G N		
1510	1530	1550
GACCTAGAAGAGTGCTTGAAATTTTGAATTTCTCAAGGACAATACATGTCTTAAAAAT		
D L E E C L K F L N F F K D N T C L K N		
1570	1590	1610
GCAATTCAAGCCTTTGGCAATGGCTCCGATGTGACCGTGTGGCAGCCAGCCTTCCCAGTA		
A I Q A F G N G S D V T V W Q P A F P V		
1630	1650	1670
CAGACCACCACTGCCACTACCACCACTGCCCTCCGGGTTAAGAACAGCCCCCTGGGGCCA		
Q T T A T T T A L R V K N K P L G P		

1690	1710	1730
GCAGGGTCTGAGAATGAAATTCCTACTCATGTGTTGGCACCGTGTGCAAAATTTACAGGCA		
A G S E N E I P T H V L P P C A N L Q A		
1750	1770	1790
CAGAAGCTGAAATCCAATGTGTCGGGCAATACACACCTCTGTATTTCCAATGGTAATTAT		
Q K L K S N V S G N T H L C I S N G N Y		
1810	1830	1850
GAAAAAGAAGGTCTCGGTGCTTCCAGCCACACATAACCCAAAAATCAATGGCTGCTCCTCCA		
E K E G L G A S S H I T T K S M A A P P		
1870	1890	1910
AGCTGTGGTCTGAGCCCACTGCTGGTCTGGTGGTAACCGCTCTGTCCACCCCTATTATCT		
S C G L S P L L V L V V T A L S T L L S		
1930	1950	1970
TTAACAGAAACATCATAGCTGCATTAAAAAATACAATATGGACATGTAAAAAGACAAAA		
L T E T S *		

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FIG.1F

1990	2010	2030
ACCAAGTTATCTGTTCCTGTTCTCTTGATAGCTGAAATCCAGTTTAGGAGCTCAGTT		
2050	2070	2090
GAGAAACAGTTCATTCACCTGGAACATTTTTTTTTT.CCTTTAAGAAAGCTTCTTGT		
2110	2130	2150
GATCCTT.GGGGCTTCTGTGAAAAACCTGATGCAGTGCTCCATCCAAACTCAGAAGGCTT		
2170	2190	2210
TGGGATATGCTGTATTTTAAAGGGACAGTTTGTAACCTGGGCTGTAAAGCAAACCTGGGGC		
2230	2250	2270
TGTGTTTCGATGATGATGAT.ATCATGAT.ATGAT.....		
2290	2310	2330
.....GATTTTAACAGTTTACTTCTGGCCCTTTCCTAGCTAGAGAAGGAG		

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FIG.1G

2350	2370	2390
TTAATATTTCTAAGGTAACCTCCCATATCTCCTTTAATGACATTGATTTCTTAATGATATAA		
2410	2430	2450
ATTTCAGCCTACATTGATGCCAAGCTTTTGGCCACAAAAGAGATTCTTACCAAGAGTGG		
2470	2490	2510
GCTTTGTGGAACACAGCTGGTACTGATGTTTCACCTTTATATATGTACTAGCATTTTCCACG		
2530	2550	
CTGATGTTTATGTACTGTAAACAGTTCTGCACTCTTGTAACAAAAGAAAA		

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FIG.2

M	F	L	A	T	L	Y	F	A	L	P	L	L	D	L	L	L	S	A	E	20
V	S	G	G	D	R	L	D	C	V	K	A	S	D	Q	C	L	K	E	Q	40
S	C	S	T	K	Y	R	T	L	R	Q	C	V	A	G	K	E	T	N	F	60
S	L	A	S	G	L	E	A	K	D	E	C	R	S	A	M	E	A	L	K	80
Q	K	S	L	Y	N	C	R	C	K	R	G	M	K	K	E	K	N	C	L	100
R	I	Y	W	S	M	Y	Q	S	L	Q	G	N	D	L	L	E	D	S	P	120
Y	E	P	V	N	S	R	L	S	D	I	F	R	V	V	P	F	I	S	D	140
V	F	Q	Q	V	E	H	I	P	K	G	N	N	C	L	D	A	A	K	A	160
C	N	L	D	D	I	C	K	K	Y	R	S	A	Y	I	T	P	C	T	T	180
S	V	S	N	D	V	C	N	R	R	K	C	H	K	A	L	R	Q	F	F	200
D	K	V	P	A	K	H	S	Y	G	M	L	F	C	S	C	R	D	I	A	220
C	T	E	R	R	R	Q	T	I	V	P	V	C	S	Y	E	E	R	E	K	240
P	N	C	L	N	L	Q	D	S	C	K	T	N	Y	I	C	R	S	R	L	260
A	D	F	F	T	N	C	Q	P	E	S	R	S	V	S	S	C	L	K	E	280
N	Y	A	D	C	L	L	A	Y	S	G	L	I	G	T	V	M	T	P	N	300
Y	I	D	S	S	S	L	S	V	A	P	W	C	D	C	S	N	S	G	N	320
D	L	E	E	C	L	K	F	L	N	F	F	K	D	N	T	C	L	K	N	340
A	I	Q	A	F	G	N	G	S	D	V	T	V	W	Q	P	A	F	P	V	360
Q	T	T	T	A	T	T	T	T	A	L	R	V	K	N	K	P	L	G	P	380
A	G	S	E	N	E	I	P	T	H	V	L	P	P	C	A	N	L	Q	A	400
Q	K	L	K	S	N	V	S	G	N	T	H	L	C	I	S	N	G	N	Y	420
E	K	E	G	L	G	A	S	S	H	I	T	T	K	S	M	A	A	P	P	440
S	C	G	L	S	P	L	L	V	L	V	V	T	A	L	S	T	L	L	S	460
L	T	E	T	S																465

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FIG.3

10 30 50
AGCTCGCTCTCCCGGGGCAGTGGTGTGGATGCACCGGAGTTCGGGCGCTGGGCAAGTTGG

70 90 110
GTCGGAAGTGAACCCCTGAAAGCGGGTCCGCCTCCCGCCCTCGCGCCCGCCCGGATCTGA

130 150 170
GTCGCTGGCGGCGGTGGGCGGCAGAGCGACGGGGAGTCTGCTCTCACCTGGATGGAGCT

190 210 230
GAACTTTGAGTGGCCAGAGGAGCGCAGTCGCCCCGGGGATCGCTGCACGCTGAGCTCTCTC

250 270 290
CCCGAGACCGGGCGGCGGCTTTGGATTTTGGGGGGGCGGGGACCAGCTGCGCGGCGGCAC

310 330 350
CATGTTCTAGCCACTCTGTACTTCGCGCTGCCACTCCTGGATTTGCTGATGTCCGCCGA
M F L A T L Y F A L P L L D L L M S A E

370 390 410
GGTGAGTGGTGGAGACCGTCTGGACTGTGTGAAAGCCAGCGATCAGTGCCTGAAGGAACA
V S G G D R L D C V K A S D Q C L K E Q

430 450 470
GAGCTGCAGCACCAAGTACCGCACACTAAGGCAGTGCCTGGCGGGCAAGGAAACCAACTT
S C S T K Y R T L R Q C V A G K E T N F

490 510 530
CAGCCTGACATCCGGCCTTGAGGCCAAGGATGAGTGCCGTAGCGCCATGGAGGCCTTGAA
S L T S G L E A K D E C R S A M E A L K

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FIG.3A

```
550          570          590
GCAGAACTCTGTACAACTGCCCGCTGCAAGCGGGCATGAAGAAAGAGAAATTTGTCT
Q K S L Y N C R C K R G M K K E K N C L

610          630          650
GCGTATCTACTGGAGCATGTACCAGAGCCTGCAGGGAATGACCTCCTGGAGATTCCCC
R I Y W S M Y Q S L Q G N D L L E D S P

670          690          710
GTATGAGCCGGTTAACAGCAGGTTGTACAGATATATCCGGGCGAGTCCCGTTCATATCAGA
Y E P V N S R L S D I F R A V P F I S D

730          750          770
TGTTTCCAGCAAGTGGAAACACATTCCCAAAGGGAACAACCTGCCTGGACGCGCAAGGC
V F Q Q V E H I S K G N N C L D A A K A

790          810          830
CTGCAACCTGGACGACACCTGTAGAAGTACAGGTGCGCCTACATCACCCCTGCACCCAC
C N L D D T C K K Y R S A Y I T P C T T
```

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FIG.3B

850 870 890
CAGCATGTCCAACGAGGTCTGCAACCGCGTAAGTGCCACAAGGCCCTCAGGCAGTTCTT
S M S N E V C N R R K C H K A L R Q F F

910 930 950
CGACAAGGTTCGGCCCAAGCACAGCTACGGGATGCTCTTCTGTCTCCTGCCGGGACATCGC
D K V P A K H S Y G M L F C S C R D I A

970 990 1010
CTGCACCGAGCGGGCGACAGACTATCGTCCCGGTGTGTCTCCTATGAAGAACGAGAGAG
C T E R R R Q T I V P V C S Y E E R E R

1030 1050 1070
GCCCAACTGCCCTGAGTCTGCAAGACTCCTGCAAGACCAATTACATCTGCAGATCTCGCCT
P N C L S L Q D S C K T N Y I C R S R L

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FIG.3C

1090 1110 1130
TGCAGATTTTATTACCAACTGCCAGCCAGAGTCAAGGTCTGTCAGCAACTGTCTTAAGGA
A D F F T N C Q P E S R S V S N C L K E

1150 1170 1190
GAACTACGCAGACTGCCCTCCTGGCCCTACTCGGGACTGATTGGCACAGTCATGACTCCCAA
N Y A D C L L A Y S G L I G T V M T P N

1210 1230 1250
CTACGTAGACTCCAGCAGCCTCAGCGTGGCACCATTGGTGTGACTGCAGCAACAGCGGCAA
Y V D S S L S V A P W C D C S N S G N

1270 1290 1310
TGACCTGGAAGACTGCTTGAAATTTCTGAATTTTTTAAGGACAATACTTGCTCTCAAAA
D L E D C L K F L N F F K D N T C L K N

1330 1350 1370
TGCAATTCAAGCCTTTGGCAATGGCTCAGATGTGACCATGTGGCAGCCAGCCCCCTCCAGT
A I Q A F G N G S D V T M W Q P A P P V

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FIG.3D

1390	1410	1430
CCAGACCACCACTGCCACCACTACCACTGCCTTCGGGTCAAGAACAAAGCCTCTGGGGCC		
Q T T A T T T A F R V K N K P L G P		
1450	1470	1490
AGCAGGGTCTGAGAATGAGATCCCCACACACGTTTACCACCCCTGTGCGAATTGCAGGC		
A G S E N E I P T H V L P P C A N L Q A		
1510	1530	1550
TCAGAAGCTGAATCCAATGTGTGGGTAGCACACACCTCTGTCTTTCTGATAGTGATT		
Q K L K S N V S G S T H L C L S D S D F		
1570	1590	1610
CGGAAGGATGGTCTCGCTGGTGCCTCCAGCCACATAACCACAAAATCAATGGCTGCTCC		
G K D G L A G A S S H I T T K S M A A P		

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FIG.3E

1630 1650 1670
TCCCAGCTGCAGTCTGAGCTCACTGCCGGTGCTGATGCTCACCGCCCTTGCTGCCCTGTT
P S C S L S S L P V L M L T A L A L L
1690 1710 1730
ATCTGTATCGTTGGCAGAAACGTCGTAGCTGCATCCGGGAAACAGTATGAAAAGACAAA
S V S L A E T S +
1750 1770 1790
AGAGAACCAAGTATTCTGTCCCTGTCCTCTTGTATATCTGAAAATCCAGTTTTAAAAGCT
1810 1830 1850
CCGTTGAGAAGCAGTTTCACCCAACTGGAACCTCTTTCCTTGTTTTAAGAAAGCTTGTTGG
1870 1890 1910
CCCTCAGGGGCTTCTGTTGAAGAACTGCTACAGGGGCTAATTCCAAACCCATAAGGCTCTG

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FIG. 3F

1930	1950	1970
GGGCGTGGTGGCGCTTAAGGGACCATTTCACCATGTAAAGCAAGCTGGGCTTATCATG		
1990	2010	2030
TGTTTGATGGTGAGGATGGTAGTGGTGATGATGGTAATTTTAACAGCTTGAACCCCTG		
2050	2070	2090
TTCTCTCTACTGGTTAGGAACAGGAGATACTATTGATAAAGATTCTTCCATGCTCTACTC		
2110	2130	
AGCAGCATTGCCTTCTGAAGACACAGGCCCGCAGCCGTCG		

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FIG.4

M F L A T L Y F A L P L L D L L M S A E 20
V S G G D R L D C V K A S D Q C L K E 40
S C S T K Y R T L R Q C V A G K E T N F 60
S L T S G L E A K D E C R S A M E A L K 80
Q K S L Y N C R C K R G M K K E K N C L 100
R I Y W S M Y Q S L Q G N D L L E D S P 120
Y E P V N S R L S D I F R A V P F I S C 140
V F Q Q V E H I S K G N N C L D A A K A 160
C N L D D T C K K Y R S A Y I T P C T T 180
S M S N E V C N R R K C H K A L R Q F F 200
D K V P A K H S Y G M L F C S C R D I A 220
C T E R R R Q T I V P V C S Y E E R E R 240
P N C L S L Q D S C K T N Y I C R S R L 260
A D F F T N C Q P E S R S V S N C L K E 280
N Y A D C L L A Y S G L I G T V M T P N 300
Y V D S S S L S V A P W C D C S N S G N 320
D L E D C L K F L N F F K D N T C L K N 340
A I Q A F G N G S D V T M W Q P A P P V 360
Q T T T A T T T T A F R V K N K P L G P 380
A G S E N E I P T H V L P P C A N L Q A 400
Q K L K S N V S G S T H L C L S D S D F 420
G K D G L A G A S S H I T T K S M A A F 440
P S C S L S S L P V L M L T A L A A L L 460
S V S L A E T S * 468

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FIG. 5

	-237		-188
Gdnfr	AATCTGGCCT	CGGAACACGC	CATTCTCCGC
Hsgr-2laf	TCTGGCCT	CGGAACACGC	CATTCTCCGC
Hsgr-2lbf	AATCTGGCCT	CGGAACACGC	CATTCTCCGC
2lacon	TCTGGCCT	CGGAACACGC	CATTCTCCGC
2lbcon	AATCTGGCCT	CGGAACACGC	CATTCTCCGC
	-187		-138
Gdnfr	ACATCCCTAA	CGAGCATCCG	AGCCGAGGGC
Hsgr-2laf	ACATCCCTAA	CGAGCATCCG	AGCCGAGGGC
Hsgr-2lbf	ACATCCCTAA	CGAGCATCCG	AGCCGAGGGC
2lacon	ACATCCCTAA	CGAGCATCCG	AGCCGAGGGC
2lbcon	ACATCCCTAA	CGAGCATCCG	AGCCGAGGGC
	-137		-88
Gdnfr	GCCCAACTCG	GCCCTTCGAG	CTCTCGAAGA
Hsgr-2laf	GCCCAACTCG	GCCCTTCGAG	CTCTCGAAGA
Hsgr-2lbf	GCCCAACTCG	GCCCTTCGAG	CTCTCGAAGA
2lacon	GCCCAACTCG	GCCCTTCGAG	CTCTCGAAGA
2lbcon	GCCCAACTCG	GCCCTTCGAG	CTCTCGAAGA

FIG. 5A

-87		-38
Gdnfr	TTCTTTT	TTCTTTTCCTA GCGCAGATAA AGTGAGCCCG GAAAGGGAAG
Hsgr-2laf	TTCTTTT	TTCTTTTCCTA GCGCAGATAA AGTGAGCCCG GAAAGGGAAG
Hsgr-2lbf	TTCTTTT	TTCTTTTCCTA GCGCAGATAA AGTGAGCCCG GAAAGGGAAG
21acon	TTCTTTT	TTCTTTTCCTA GCGCAGATAA AGTGAGCCCG GAAAGGGAAG
21bcon	TTCTTTT	TTCTTTTCCTA GCGCAGATAA AGTGAGCCCG GAAAGGGAAG
-37		12
Gdnfr	GAGGGGGCGG	GGACACCAT
Hsgr-2laf	GAGGGGGCGG	GGACACCAT
Hsgr-2lbf	GAGGGGGCGG	GGACACCAT
21acon	GAGGGGGCGG	GGACACCAT
21bcon	GAGGGGGCGG	GGACACCAT
13		62
Gdnfr	AACTGGCTCC	TCGCCGCAGC TGGACGCGGT CGGTTGAGTC CAGGTTGGGT
Hsgr-2laf	AACTGGCTCC	TCGCCGCAGC TGGACGCGGT CGGTTGAGTC CAGGTTGGGT
Hsgr-2lbf	AACTGGCTCC	TCGCCGCAGC TGGACGCGGT CGGTTGAGTC CAGGTTGGGT
21acon	AACTGGCTCC	TCGCCGCAGC TGGACGCGGT CGGTTGAGTC CAGGTTGGGT
21bcon	AACTGGCTCC	TCGCCGCAGC TGGACGCGGT CGGTTGAGTC CAGGTTGGGT

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FIG. 5B

	63		112
Gdnfr	CGGACCTGAA	CCCCTAAAG	CGGAACCGCC
			TCCCGCCCTC
			GCCATCCCGG
Hsgr-21af	CGGACCTGAA	CCCCTAAAG	CGGAACCGCC
			TCCCGCCCTC
			GCCATCCCGG
Hsgr-21bf	CGGACCTGAA	CCCCTAAAG	CGGAACCGCC
			TCCCGCCCTC
			GCCATCCCGG
21acon	CGGACCTGAA	CCCCTAAAG	CGGAACCGCC
			TCCCGCCCTC
			GCCATCCCGG
21bcon	CGGACCTGAA	CCCCTAAAG	CGGAACCGCC
			TCCCGCCCTC
			GCCATCCCGG
	113		162
Gdnfr	AGCTGAGTCG	CCGGCGGCGG	TGGCTGCTGC
			CAGACCCGGA
			GTTTCCTCTT
Hsgr-21af	AGCTGAGTCG	CCGGCGGCGG	TGGCTGCTGC
			CAGACCCGGA
			GTTTCCTCTT
Hsgr-21bf	AGCTGAGTCG	CCGGCGGCGG	TGGCTGCTGC
			CAGACCCGGA
			GTTTCCTCTT
21acon	AGCTGAGTCG	CCGGCGGCGG	TGGCTGCTGC
			CAGACCCGGA
			GTTTCCTCTT
21bcon	AGCTGAGTCG	CCGGCGGCGG	TGGCTGCTGC
			CAGACCCGGA
			GTTTCCTCTT
	163		212
Gdnfr	TCACTGGATG	GAGCTGAACT	TTGGGCGGCC
			AGAGCAGCAC
			AGCTGTCCGG
Hsgr-21af	TCACTGGATG	GAGCTGAACT	TTGGGCGGCC
			AGAGCAGCAC
			AGCTGTCCGG
Hsgr-21bf	TCACTGGATG	GAGCTGAACT	TTGGGCGGCC
			AGAGCAGCAC
			AGCTGTCCGG
21acon	TCACTGGATG	GAGCTGAACT	TTGGGCGGCC
			AGAGCAGCAC
			AGCTGTCCGG
21bcon	TCACTGGATG	GAGCTGAACT	TTGGGCGGCC
			AGAGCAGCAC
			AGCTGTCCGG

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FIG. 5C

	213		262
Gdnfr	GGATCGCTGC	ACGCTGAGCT	CCCTCGGCCAA GACCCAGCGG CGGCTCGGGA
Hsgr-2laf	GGATCGCTGC	ACGCTGAGCT	CCCTCGGCCAA GACCCAGCGG CGGCTCGGGA
Hsgr-2lbf	GGATCGCTGC	ACGCTGAGCT	CCCTCGGCCAA GACCCAGCGG CGGCTCGGGA
2lacon	GGATCGCTGC	ACGCTGAGCT	CCCTCGGCCAA GACCCAGCGG CGGCTCGGGA
2lbcon	GGATCGCTGC	ACGCTGAGCT	CCCTCGGCCAA GACCCAGCGG CGGCTCGGGA
	263		312
Gdnfr	TTTTTTTGGG	GGGGCGGGGA	CCAGCCCCGC GCCGGCACCA TGTTCCCTGGC
Hsgr-2laf	TTTTTTTGGG		
Hsgr-2lbf	TTTTTTTGGG		
2lacon	TTTTTTTGGG	GGGGCGGGGA	CCAGCCCCGC GCCGGCACCA TGTTCCCTGGC
2lbcon	TTTTTTTGGG	GGGGCGGGGA	CCAGCCCCGC GCCGGCACCA TGTTCCCTGGC
	313		362
Gdnfr	GACCCGTGAC	TTCCGGCTGC	CGCTCTTGGA CTTGCTCCTG TCGGCCGAAG
2lacon	GNCCCTGTAC	TTCCGGCTGC	CGCTCTTGGA CTTGCTCCTG TCGGCCGAAG
2lbcon	GACCCGTGAC	TTCCGGCTGC	CGCTCTTGGA CTTGCTCCTG TCGGCCGAAG

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FIG.5D

```
363                                     412
Gdnfr TGAGCGGCGG AGACCGCCTG GATTGCGTGA AAGCCAGTGA TCAGTGCCTG
21acon TGAGCGGCGG AGACCGCCTG GATTGCGTGA AAGCCAGTGA TCAGTGCCTG
21bcon TGAGCGGCGG AGACCGCCTG GATTGCGTGA AAGCCAGTGA TCAGTGCCTG

413                                     462
Gdnfr AAGGAGCAGA GCTGCAGCAC CAAGTACCGC ACGCTAAGGC AGTGCCTGGC
21acon AAGGAGCAGA GCTGCAGCAC CAAGTACCGC ACGCTAAGGC AGTGCCTGGC
21bcon AAGGAGCAGA GCTGCAGCAC CAAGTACCGC ACGCTAAGGC AGTGCCTGGC

463                                     512
Gdnfr GGGCAAGGAG ACCAACTTCA GCCTGGCATC CGGCCTGGAG GCCAAGGATG
21acon GGGCAAGGAG ACCAACTTCA GCCTGGCATC CGGCCTGGAG GCCAAGGATG
21bcon GGGCAAGGAG ACCAACTTCA GCCTGGCATC CGGCCTGGAG GCCAAGGATG

513                                     562
Gdnfr AGTGCCGCAG CGCCATGGAG GCCCTGAAGC AGAAGTCGCT CTACAACTGC
21acon AGTGCCGCAG CGCCATGGAG GCCCTGAAGC AGAAGTCGCT CTACAACTGC
21bcon AGTGCCGCAG CGCCATGGAG GCCCTGAAGC AGAAGTCGCT CTACAACTGC
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FIG.5E

563	612
Gdnfr	CGCTGCAAGC GGGGTATGAA GAAGGAGAAG AACTGCCTGC GCATTACTG
21acon	CGCTGCAAGC GGGGTATGAA GAAGGAGAAG AACTGCCTGC GCATTACTG
21bcon	CGCTGCAAGC GGGGTATGAA GAAGGAGAAG AACTGCCTGC GCATTACTG
613	662
Gdnfr	GAGCATGTAC CAGAGCCTGC AGGGAATGA TCTGCTGGAG GATTCCCCAT
21acon	GAGCATGTAC CAGAGCCTGC AGGGAATGA TCTGCTGGAG GATTCCCCAT
21bcon	GAGCATGTAC CAGAGCCTGC AGGGAATGA TCTGCTGGAG GATTCCCCAT
663	712
Gdnfr	ATGAACCCAGT TAACAGCAGA TTGTCAGATA TATTCCGGGT GGTCCCATTTC
21acon	ATGAACCCAGT TAACAGCAGA TTGTCAGATA TATTCCGGGT GGTCCCATTTC
21bcon	ATGAACCCAGT TAACAGCAGA TTGTCAGATA TATTCCGGGT GGTCCCATTTC
713	762
Gdnfr	ATATCAGATG TTTTTCAGCA AGTGGAGCAC ATTCCCAAAG GGAACAACCTG
21acon	ATATCAGATG TTTTTCAGCA AGTGGAGCAC ATTCCCAAAG GGAACAACCTG
21bcon	ATATCAGATG TTTTTCAGCA AGTGGAGCAC ATTCCCAAAG GGAACAACCTG

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FIG.5F

	763		812
Gdnfr	CCTGGATGCA	GCGAAGGCCT	GCAACCTCGA CGACATTTC AAGAAGTACA
21acon	CCTGGATGCA	GCGAAGGCCT	GCAACCTCGA CGACATTTC AAGAAGTACA
21bcon	CCTGGATGCA	GCGAAGGCCT	GCAACCTCGA CGACATTTC AAGAAGTACA
	813		862
Gdnfr	GGTCGGCGTA	CATCACCCCG	TGCACCACCA GCGTGTCCAA .GATGTCTGC
Hsgr-29a	GGTCGGCGTA	CATCACCCCG	TGCACCACCA GCGTGTCCAA TGATGTCTGC
21acon	GGTCGGCGTA	CATCACCCCG	TGCACCACCA GCGTGTCCAA CGATGTCTGC
21bcon	GGTCGGCGTA	CATCACCCCG	TGCACCACCA GCGTGTCCAA CGATGTCTGC
29brc	GGTCGGCGTA	CATCACCCCG	TGCACCACCA GCGTGTCCAA TGATGTCTGC
	863		912
Gdnfr	AACCGCCGCA	AGTGCCACAA	GGCCCTCCGG CAGTTCTTTG ACAAGGTCCC
Hsgr-29a	AACCGCCGCA	AGTGCCACAA	GGCCCTCCGG CAGTTCTTTG ACAAGGTCCC
21acon	AACCGCCGCA	AGTGCCACAA	GGCCCTCCGG CAGTTCTTTG ACAAGGTCCC
21bcon	AACCGCCGCA	AGTGCCACAA	GGCCCTCCGG CAGTTCTTTG ACAAGGTCCC
29brc	AACCGCCGCA	AGTGCCACAA	GGCCCTCCGG CAGTTCTTTG ACAAGGTCCC

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FIG. 5G

913			962
Gdnfr	GGCCAAGCAC AGCTACGGAA TGCTCTTCTG CTCTTGCCGG GACATCGCCT		
Hsgr-29a	GGCCAAGCAC AGCTACGGAA TGCTCTTCTG CTCTTGCCGG GACATCGCCT		
21acon	GGCCAAGCAC AGCTACGGAA TGCTCTTCTG CTCTTGCCGG GACATCGCCT		
21bcon	GGCCAAGCAC AGCTACGGAA TGCTCTTCTG CTCTTGCCGG GACATCGCCT		
29brc	GGCCAAGCAC AGCTACGGAA TGCTCTTCTG CTCTTGCCGG GACATCGCCT		
	963		1012
Gdnfr	GCACAGAGCG GAGGCGACAG ACCATCGTGC CTGTGTGCTC CTATGAAGAG		
Hsgr-29a	GCACAGAGCG GAGGCGACAG ACCATCGTGC CTGTGTGCTC CTATGAAGAG		
21acon	GCACAGAGCG GAGGCGACAG ACCATCGTGC CTGTGTGCTC CTATGAAGAG		
21bcon	GCACAGAGCG GAGGCGACAG ACCATCGTGC CTGTGTGCTC CTATGAAGAG		
29brc	GCACAGAGCG GAGGCGACAG ACCATCGTGC CTGTGTGCTC CTATGAAGAG		
	1013		1062
Gdnfr	AGGGAGAAGC CCAACTGTTT GAATTGCGAG GACTCCTGCA AGACGAATTA		
Hsgr-21ar		GAATTGCGAG GACTCCTGCA AGACGAATTA	
Hsgr-21br			A
Hsgr-29a	AGGGAGAAGC CCAACTGTTT GAATTGCGAG GACTCCTGCA AGACGAATTA		
21acon	AGGGAGAAGC CCAACTGTTT GAATTGCGAG GACTCCTGCA AGACGAATTA		
21bcon	AGGGAGAAGC CCAACTGTTT GAATTGCGAG GACTCCTGCA AGACGAATTA		
29brc	AGGGAGAAGC CCAACTGTTT GAATTGCGAG GACTCCTGCA AGACGAATTA		

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FIG.5H

1063		1112
Gdnfr	CATCTGCAGA TCTCGCCTTG CGGATTTTTT TACCAACTGC CAGCCAGAGT	
Hsgr-21ar	CATCTGCAGA TCTCGCCTTG CGGATTTTTT TACCAACTGC CAGCCAGAGT	
Hsgr-21br	CATCTGCAGA TCTCGCCTTG CGGATTTTTT TACCAACTGC CAGCCAGAGT	
Hsgr-29a	CATCTGCAGA TCTCGCCTTG CGGATTTTTT TACCAACTGC CAGCCAGAGT	
21acon	CATCTGCAGA TCTCGCCTTG CGGATTTTTT TACCAACTGC CAGCCAGAGT	
21bcon	CATCTGCAGA TCTCGCCTTG CGGATTTTTT TACCAACTGC CAGCCAGAGT	
29brc	CATCTGCAGA TCTCGCCTTG CGGATTTTTT TACCAACTGC CAGCCAGAGT	
1113		1162
Gdnfr	CAAGGTCTGT CAGCAGCTGT CTAAAGGAAA ACTACGCTGA CTGCCTCCTC	
Hsgr-21ar	CAAGGTCTGT CAGCAGCTGT CTAAAGGAAA ACTACGCTGA CTGCCTCCTC	
Hsgr-21br	CAAGGTCTGT CAGCAGCTGT CTAAAGGAAA ACTACGCTGA CTGCCTCCTC	
Hsgr-29a	CAAGGTCTGT CAGCAGCTGT CTAAAGGAAA ACTACGCTGA CTGCCTCCTC	
21acon	CAAGGTCTGT CAGCAGCTGT CTAAAGGAAA ACTACGCTGA CTGCCTCCTC	
21bcon	CAAGGTCTGT CAGCAGCTGT CTAAAGGAAA ACTACGCTGA CTGCCTCCTC	
29brc	CAAGGTCTGT CAGCAGCTGT CTAAAGGAAA ACTACGCTGA CTGCCTCCTC	

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FIG. 5I

	1163		1212
Gdnfr	GCCTACTCGG GGCTTATTGG CACAGTCATG ACCCCCAACT ACATAGACTC		
Hsgr-21ar	GCCTACTCGG GGCTTATTGG CACAGTCATG ACCCCCAACT ACATAGACTC		
Hsgr-21br	GCCTACTCGG GGCTTATTGG CACAGTCATG ACCCCCAACT ACATAGACTC		
Hsgr-29a	GCCTACTCGG GGCTTATTGG CACAGTCATG ACCCCCAACT ACATAGACTC		
21acon	GCCTACTCGG GGCTTATTGG CACAGTCATG ACCCCCAACT ACATAGACTC		
21bcon	GCCTACTCGG GGCTTATTGG CACAGTCATG ACCCCCAACT ACATAGACTC		
29brc	GCCTACTCGG GGCTTATTGG CACAGTCATG ACCCCCAACT ACATAGACTC		
	1213		1262
Gdnfr	CAGTAGCCTC AGTGTGGCCC CATGGTGTGA CTGCAGCAAC AGTGGGAACG		
Hsgr-2		TGGGAACG	
Hsgr-21ar	CAGTAGCCTC AGTGTGGCCC CATGGTGTGA CTGCAGCAAC AGTGGGAACG		
Hsgr-21br	CAGTAGCCTC AGTGTGGCCC CATGGTGTGA CTGCAGCAAC AGTGGGAACG		
Hsgr-29a	CAGTAGCCTC AGTGTGGCCC CATGGTGTGA CTGCAGCAAC AGTGGGAACG		
21acon	CAGTAGCCTC AGTGTGGCCC CATGGTGTGA CTGCAGCAAC AGTGGGAACG		
21bcon	CAGTAGCCTC AGTGTGGCCC CATGGTGTGA CTGCAGCAAC AGTGGGAACG		
29brc	CAGTAGCCTC AGTGTGGCCC CATGGTGTGA CTGCAGCAAC AGTGGGAACG		

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FIG.5J

1263		1312
Gdnfr	ACCTAGAAGA GTGCTTGAAA TTTTGAATT TCTTCAAGGA CAATACATGT	
Hsgr-2	ACCTAGAAGA GTGCTTGAAA TTTTGAATT TCTTCAAGGA CAATACATGT	
Hsgr-9	A GTGCTTGAAA TTTTGAATT TCTTCAAGGA CAATACATGT	
Hsgr-21ar	ACCTAGAAGA GTGCTTGAAA TTTTGAATT TCTTCAAGGA CAATACATGT	
Hsgr-21br	ACCTAGAAGA GTGCTTGAAA TTTTGAATT TCTTCAAGGA CAATACATGT	
Hsgr-29a	ACCTAGAAGA GTGCTTGAAA TTTTGAATT TCTTCAAGGA CAATACATGT	
21acon	ACCTAGAAGA GTGCTTGAAA TTTTGAATT TCTTCAAGGA CAATACATGT	
21bcon	ACCTAGAAGA GTGCTTGAAA TTTTGAATT TCTTCAAGGA CAATACATGT	
29brc	ACCTAGAAGA GTGCTTGAAA TTTTGAATT TCTTCAAGGA CAATACATGT	
1313		1362
Gdnfr	CTTAAAAATG CAATTCAAGC CTTTGGCAAT GGCTCCGATG TGACCGTGTG	
Hsgr-2	CTTAAAAATG CAATTCAAGC CTTTGGCAAT GGCTCCGATG TGACCGTGTG	
Hsgr-9	CTTAAAAATG CAATTCAAGC CTTTGGCAAT GGCTCCGATG TGACCGTGTG	
Hsgr-21ar	CTTAAAAATG CAATTCAAGC CTTTGGCAAT GGCTCCGATG TGACCGTGTG	
Hsgr-21br	CTTAAAAATG CAATTCAAGC CTTTGGCAAT GGCTCCGATG TGACCGTGTG	
Hsgr-29a	CTTAAAAATG CAATTCAAGC CTTTGGCAAT GGCTCCGATG TGACCGTGTG	
21acon	CTTAAAAATG CAATTCAAGC CTTTGGCAAT GGCTCCGATG TGACCGTGTG	
21bcon	CTTAAAAATG CAATTCAAGC CTTTGGCAAT GGCTCCGATG TGACCGTGTG	
29brc	CTTAAAAATG CAATTCAAGC CTTTGGCAAT GGCTCCGATG TGACCGTGTG	

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FIG. 5K

1363		1412
Gdnfr	GCAGCCAGCC TTCCCAGTAC AGACCACCAC TGCCaCTACC ACCACTGCCC	
Hsgr-2	GCAGCCAGCC TTCCCAGTAC AGACCACCAC TGCCACTACC ACCACTGCCC	
Hsgr-9	GCAGCCAGCC TTCCCAGTAC AGACCACCAC TGCCACTACC ACCACTGCCC	
Hsgr-21ar	GCAGCCAGCC TTCCCAGTAC AGACCACCAC TGCCACTACC ACCACTGCCC	
Hsgr-21br	GCAGCCAGCC TTCCCAGTAC AGACCACCAC TGCCACTACC ACCACTGCCC	
Hsgr-29a	GCAGCCAGCC TTCCCAGTAC AGACCACCAC TGCCGCTACC ACCACTGCCC	
21acon	GCAGCCAGCC TTCCCAGTAC AGACCACCAC TGCCACTACC ACCACTGCCC	
21bcon	GCAGCCAGCC TTCCCAGTAC AGACCACCAC TGCCACTACC ACCACTGCCC	
29brc	GCAGCCAGCC TTCCCAGTAC AGACCACCAC TGCCGCTACC ACCACTGCCC	
	1413	1462
Gdnfr	TCCGGGTAA GAACAAGCCC CTGGGGCCAG CAGGGTCTGA GAATGAAATT	
Hsgr-2	TCCGGGTAA GAACAAGCCC CTGGGGCCAG CAGGGTCTGA GAATGAAATT	
Hsgr-9	TCCGGGTAA GAACAAGCCC CTGGGGCCAG CAGGGTCTGA GAATGAAATT	
Hsgr-21ar	TCCGGGTAA GAACAAGCCC CTGGGGCCAG CAGGGTCTGA GAATGAAATT	
Hsgr-21br	TCCGGGTAA GAACAAGCCC CTGGGGCCAG CAGGGTCTGA GAATGAAATT	
Hsgr-29a	TCCGGGTAA GAACAAGCCC CTGGGGCCAG CAGGGTCTGA GAATGAAATT	
21acon	TCCGGGTAA GAACAAGCCC CTGGGGCCAG CAGGGTCTGA GAATGAAATT	
21bcon	TCCGGGTAA GAACAAGCCC CTGGGGCCAG CAGGGTCTGA GAATGAAATT	
29brc	TCCGGGTAA GAACAAGCCC CTGGGGCCAG CAGGGTCTGA GAATGAAATT	

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FIG. 5L

	1463		1512
Gdnfr	CCCACTCATG	TTTTGCCACC	GTGTGCAAAAT TTACAGGCAC AGAAGCTGAA
Hsgr-2	CCCACTCATG	TTTTGCCACC	GTGTGCAAAAT TTACAGGCAC AGAAGCTGAA
Hsgr-9	CCCACTCATG	TTTTGCCACC	GTGTGCAAAAT TTACAGGCAC AGAAGCTGAA
Hsgr-21ar	CCCACTCATG	TTTTGCCACC	GTGTGCAAAAT TTACAGGCAC AGAAGCTGAA
Hsgr-21br	CCCACTCATG	TTTTGCCACC	GTGTGCAAAAT TTACAGGCAC AGAAGCTGAA
Hsgr-29a	CCCACTCATG	TTTTGCCACC	GTGTGCAAAAT TTACAGGCAC AGAAGCTGAA
21acon	CCCACTCATG	TTTTGCCACC	GTGTGCAAAAT TTACAGGCAC AGAAGCTGAA
21bcon	CCCACTCATG	TTTTGCCACC	GTGTGCAAAAT TTACAGGCAC AGAAGCTGAA
29brc	CCCACTCATG	TTTTGCCACC	GTGTGCAAAAT TTACAGGCAC AGAAGCTGAA
	1513		1562
Gdnfr	ATCCAATGTG	TCGGGCAATA	CACACCTCTG TATTTCCAAT GGTAATTATG
Hsgr-2	ATCCAATGTG	TCGGGCAATA	CACACCTCTG TATTTCCAAT GGTAATTATG
Hsgr-9	ATCCAATGTG	TCGGGCAATA	CACACCTCTG TATTTCCAAT GGTAATTATG
Hsgr-21ar	ATCCAATGTG	TCGGGCAATA	CACACCTCTG TATTTCCAAT GGTAATTATG
Hsgr-21br	ATCCAATGTG	TCGGGCAATA	CACACCTCTG TATTTCCAAT GGTAATTATG
21acon	ATCCAATGTG	TCGGGCAATA	CACACCTCTG TATTTCCAAT GGTAATTATG
21bcon	ATCCAATGTG	TCGGGCAATA	CACACCTCTG TATTTCCAAT GGTAATTATG
29brc	ATCCAATGTG	TCGGGCAATA	CACACCTCTG TATTTCCAAT GGTAATTATG

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FIG. 5M

	1563		1612
Gdnfr	AAAAGAAGG TCTCGGTGCT TCCAGCCACA TAACCACAAA ATCAATGGCT		
Hsgr-2	AAAAGAAGG TCTCGGTGCT TCCAGCCACA TAACCACAAA ATCAATGGCT		
Hsgr-9	AAAAGAAGG TCTCGGTGCT TCCAGCCACA TAACCACAAA ATCAATGGCT		
Hsgr-21ar	AAAAGAAGG TCTCGGTGCT TCCAGCCACA TAACCACAAA ATCAATGGCT		
Hsgr-21br	AAAAGAAGG TCTCGGTGCT TCCAGCCACA TAACCACAAA ATCAATGGCT		
21acon	AAAAGAAGG TCTCGGTGCT TCCAGCCACA TAACCACAAA ATCAATGGCT		
21bcon	AAAAGAAGG TCTCGGTGCT TCCAGCCACA TAACCACAAA ATCAATGGCT		
29brc	AAAAGAAGG TCTCGGTGCT TCCAGCCACA TAACCACAAA ATCAATGGCT		
	1613		1662
Gdnfr	GCTCCTCCAA GCTGTGGTCT GAGCCCACTG CTGGTCCTGG TGGTAACCGC		
Hsgr-2	GCTCCTCCAA GCTGTGGTCT GAGCCCACTG CTGGTCCTGG TGGTAACCGC		
Hsgr-9	GCTCCTCCAA GCTGTGGTCT GAGCCCACTG CTGGTCCTGG TGGTAACCGC		
Hsgr-21ar	GCTCCTCCAA GCTGTGGTCT GAGCCCACTG CTGGTCCTGG TGGTAACCGC		
Hsgr-21br	GCTCCTCCAA GCTGTGGTCT GAGCCCACTG CTGGTCCTGG TGGTAACCGC		
21acon	GCTCCTCCAA GCTGTGGTCT GAGCCCACTG CTGGTCCTGG TGGTAACCGC		
21bcon	GCTCCTCCAA GCTGTGGTCT GAGCCCACTG CTGGTCCTGG TGGTAACCGC		
29brc	GCTCCTCCAA GCTGTGGTCT GAGCCCACTG CTGGTCCTGG TGGTAACCGC		

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FIG. 5N

1663	1712
Gdnfr	TCTGTCCACC CTATTATCTT TAACAGAAAC ATCATAGCTG CATTAAAAAA
Hsgr-2	TCTGTCCACC CTATTATCTT TAACAGAAAC ATCATAGCTG CATTAAAAAA
Hsgr-9	TCTGTCCACC CTATTATCTT TAACAGAAAC ATCATAGCTG CATTAAAAAA
Hsgr-21ar	TCTGTCCACC CTATTATCTT TAACAGAAA
Hsgr-21br	TCTGTCCACC CTATTATCTT TAACAGAAA
21acon	TCTGTCCACC CTATTATCTT TAACAGAAA
21bcon	TCTGTCCACC CTATTATCTT TAACAGAAA
29brc	TCTGTCCACC CTATTATCTT TAACAGAAAC ATCATAGCTG CATTAAAAAA
1713	1762
Gdnfr	ATACAATATG GACATGTAAA AAGACAAAAA CCAAGTTATC TGTTTCCTGT
Hsgr-2	ATACAATATG GACATGTAAA AAGACAAAAA CCAAGTTATC TGTTTCCTGT
Hsgr-9	ATACAATATG GACATGTAAA AAGACAAAAA CCAAGTTATC TGTTTCCTGT
29brc	ATACAATATG GACATGTAAA AAGACAAAAA CCAAGTTATC TGTTTCCTGT
1763	1812
Gdnfr	TCTCTTGTAT AGCTGAAATT CCAGTTTAGG AGCTCAGTTG AGAAACAGTT
Hsgr-2	TCTCTTGTAT AGCTGAAATT CCAGTTTAGG AGCTCAGTTG AGAAACAGTT
Hsgr-9	TCTCTTGTAT AGCTGAAATT CCAGTTTAGG AGCTCAGTTG AGAAACAGTT
29brc	TCTCTTGTAT AGCTGAAATT CCAGTTTAGG AGCTCAGTTG AGAAACAGTT

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FIG.50

1813		1862
Gdnfr	CCATTCAACT GGAACATTTT TTTTTT.CC TTTTAAGAAA GCTTCTTG TG	
Hsgr-2	CCATTCAACT GGAACATTTT TTTTTT.CC TTTTAAGAAA GCTTCTTG TG	
Hsgr-9	CCATTCAACT GGAACATTTT TTTTTTTCC TTTTAAGAAA GCTTCTTG TG	
29brc	CCATTCAACT GGAACATTTT TTTTTT.CC TTTTAAGAAA GCTTCTTG TG	
1863		1912
Gdnfr	ATCCTTCGGG GCTTCTGTGA AAAACCTGAT GCAGTGCTCC ATCCAAACTC	
Hsgr-2	ATCCTTCGGG GCTTCTGTGA AAAACCTGAT GCAGTGCTCC ATCCAAACTC	
Hsgr-9	ATCCTTTGGG GCTTCTGTGA AAAACCTGAT GCAGTGCTCC ATCCAAACTC	
29brc	ATCCTTCGGG GCTTCTGTGA AAAACCTGAT GCAGTGCTCC ATCCAAACTC	
1913		1962
Gdnfr	AGAAGGCTTT GGGATATGCT GTATTTTAAA GGGACAGTTT GTAAC TTGGG	
Hsgr-2	AGAAGGCTTT GGGATATGCT GTATTTTAAA GGGACAGTTT GTAAC TTGGG	
Hsgr-9	AGAAGGCTTT GGGATATGCT GTATTTTAAA GGGACAGTTT GTAAC TTGGG	
29brc	AGAAGGCTTT GGGATATGCT GTATTTTAAA GGGACAGTTT GTAAC TTGGG	

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FIG.5P

1963		2012
Gdnfr	CTGTAAAGCA AACTGGGGCT GTGTTTTCGA TGATGATGAT CATCATGATC	
Hsgr-2	CTGTAAAGCA AACTGGGGCT GTGTTTTCGA TGATGATGAT CATCATGATC	
Hsgr-9	CTGTAAAGCA AACTGGGGCT GTGTTTTCGA TGATGATGAT CATCATGATG	
29brc	CTGTAAAGCA AACTGGGGCT GTGTTTTCGA TGATGATGAT CATCATGATC	
2013		2062
Gdnfr	ATGAT.....GATTTT
Hsgr-2	ATGAT.....GATTTT
Hsgr-9	ATGATCATCA TGATCATGAT GATGATCATC ATGATCATGA TGATGATTTT	
29brc	ATGAT.....GATTTT
2063		2112
Gdnfr	AACAGTTTTA CTTCTGGCCT TTCCTAGCTA GAGAAGGAGT TAATATTTCT	
Hsgr-2	AACAGTTTTA CTTCTGGCCT TTCCTAGCTA GAGAAGGAGT TAATATTTCT	
Hsgr-9	AACAGTTTTA CTTCTGGCCT TTCCTAGCTA GAGAAGGAGT TAATATTTCT	
29brc	AACAGTTTTA CTTCTGGCCT TTCCTAGCTA GAGAAGGAGT TAATATTTCT	

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FIG. 5Q

2113	2162
Gdnfr AAGGTAAGTC CCATATCTCC TTTAATGACA TTGATTTCTA ATGATATAAA	
Hsgr-2 AAGGTAAGTC CCATATCTCC TTTAATGACA TTGATTTCTA ATGATATAAA	
Hsgr-9 AAGGTAAGTC CCATATCTCC TTTAATGACA TTGATTTCTA ATGATATAAA	
29brc AAGGTAAGTC CCATATCTCC TTTAATGACA TTGATTTCTA ATGATATAAA	
2163	2212
Gdnfr TTTCAGCCTA CATTGATGCC AAGCTTTTTT GCCACAAAGA AGATTCTTAC	
Hsgr-2 TTTCAGCCTA CATTGATGCC AAGCTTTTTT GCCACAAAGA AGATTCTTAC	
Hsgr-9 TTTCAGCCTA CATTGATGCC AAGCTTTTTT GCCACAAAGA AGATTCTTAC	
29brc TTTCAGCCTA CATTGATGCC AAGCTTTTTT GCCACAAAGA AGATTCTTAC	
2213	2262
Gdnfr CAAGAGTGGG CTTTGTGGAA ACAGCTGGTA CTGATGTTCA CCTTTATATA	
Hsgr-2 CAAGAGTGGG CTTTGTGGAA ACAGCTGGTA CTGATGTTCA CCTTTATATA	
Hsgr-9 CAAGAGTGGG CTTTGTGGAA ACAGCTGGTA CTGATGTTCA CCTTTATATA	
29brc CAAGAGTGGG CTTTGTGGAA ACAGCTGGTA CTGATGTTCA CCTTTATATA	

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FIG.5R

	2263		2312
Gdnfr	TGTA TAGCA	TTTTCCACGC	TGATGTTTAT
			GTACTGTAAA
			CAGTTCTGCA
Hsgr-2	TGTA TAGCA	TTTTCCACGC	TGATGTTTAT
			GTACTGTAAA
			CAGTTCTGCA
Hsgr-9	TGTA TAGCA	TTTTCCACGC	TGATGTTTAT
			GTACTGTAAA
			CAGTTCTGCA
29brc	TGTA TAGCA	TTTTCCACGC	TGATGTTTAT
			GTACTGTAAA
			CAGTTCTGCA
	2313		2362
Gdnfr	CTCTTG TACA	AAAGAAAAAA	CACCTGTCAC
			ATCCAAATAT
			AGTATCTGTC
Hsgr-2	CTCTTG TACA	AAAGAAAA	
Hsgr-9	CTCTTG TACA	AAAGAAAA	
29brc	CTCTTG TACA	AAAGAAAAAA	CACCTGTCAC
			ATCCAAATAT
			AGTATCTGTC
	2363		2412
Gdnfr	TTTTTC GTCAA	AATAGAGAGT	GGGGAATGAG
			TGTGCCGATT
			CAATACCTCA
29brc	TTTTTC GTCAA	AATAGAGAGT	GGGGAATGAG
			TGTGCCGATT
			CAATACCTCA
	2413		2462
Gdnfr	ATCCCTGAAC	GACACTCTCC	TAATCCTAAG
			CCTTACCTGA
			GTGAGAAGCC
29brc	ATCCCTGAAC	GACACTCTCC	TAATCCTAAG
			CCTTACCTGA
			GTGAGAAGCC

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FIG.5S

2463	2512
Gdnfr CTTTACCTAA CAAAAGTCCA ATATAGCTGA AATGTCGCTC TAATACTCTT	
29brc CTTTACCTAA CAAAAGTCCA ATATAGCTGA AATGTCGCTC TAATACTCTT	
2513	2562
Gdnfr TACACATATG AGGTTATATG TAGAAAAAAA TTTTACTACT AAATGATTTC	
29brc TACACATATG AGGTTATATG TAGAAAAAAA TTTTACTACT AAATGATTTC	
2563	2612
Gdnfr AACTATTGGC TTTCTATATT TTGAAAGTAA TGATATTGTC TCATTTT	
29brc AACTATTGGC TTTCTATATT TTGAAAGTAA TGATATTGTC TCATTTT	
2613	2662
Gdnfr ACTGATGGTT TAATACAAA TACACAGAGC TTGTTTCCCC TCATAAGTAG	
29brc ACTGATGGTT TAATACAAA TACACAGAGC TTGTTTCCCC TCATAAGTAG	

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FIG. 5T

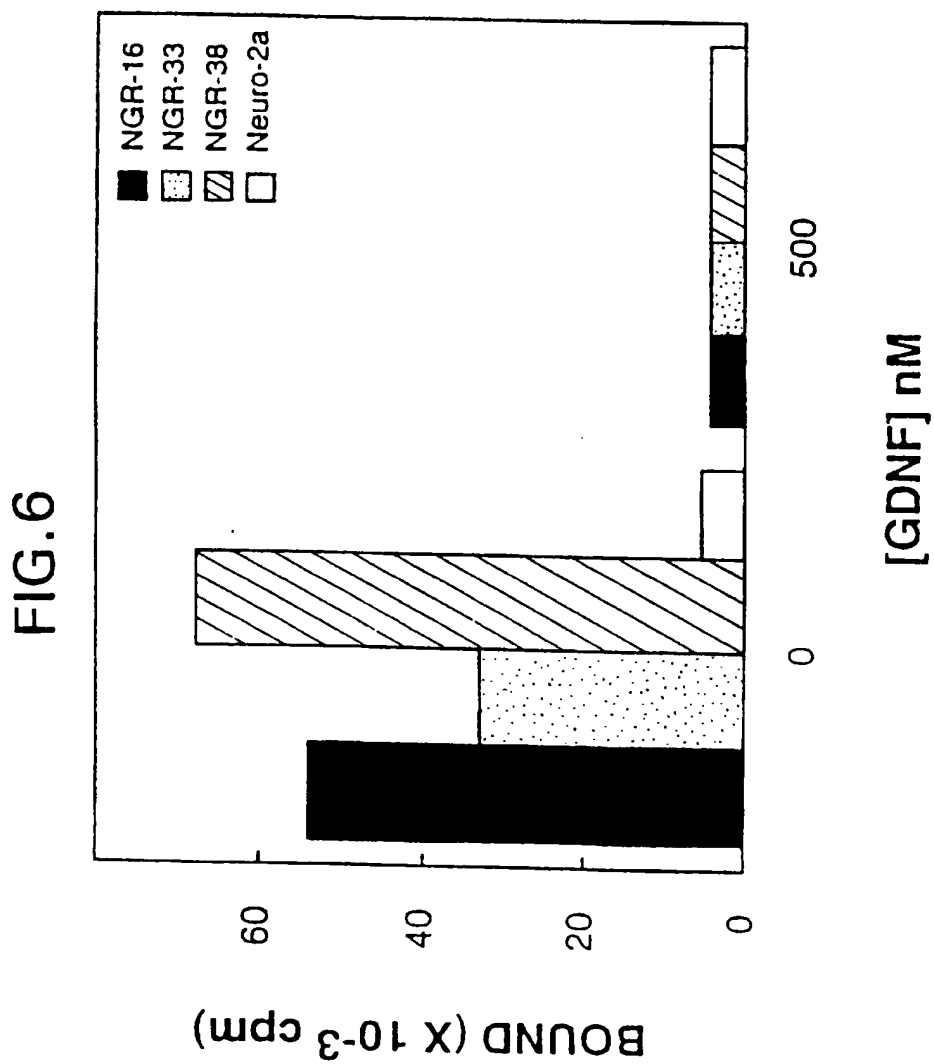
2663	2712
Gdnfr TGTTGCTCT GATATGAACT TCACAAATAC AGCTCATCAA AAGCAGACTC	
29brc TGTTGCTCT GATATGAACT TCACAAATAC AGCTCATCAA AAGCAGACTC	
2713	2762
Gdnfr TGAGAAGCCT CGTGCTGTAG CAGAAAGTTC TGCATCATGT GACTGTGGAC	
29brc TGAGAAGCCT CGTGCTGTAG CAGAAAGTTC TGCATCATGT GACTGTGGAC	
2763	2812
Gdnfr AGGCAGGAGG AAACAGAACA GACAAGCATT GTCTTTTGTG ATTGCTCGAA	
29brc AGGCAGGAGG AAACAGAACA GACAAGCATT GTCTTTTGTG ATTGCTCGAA	

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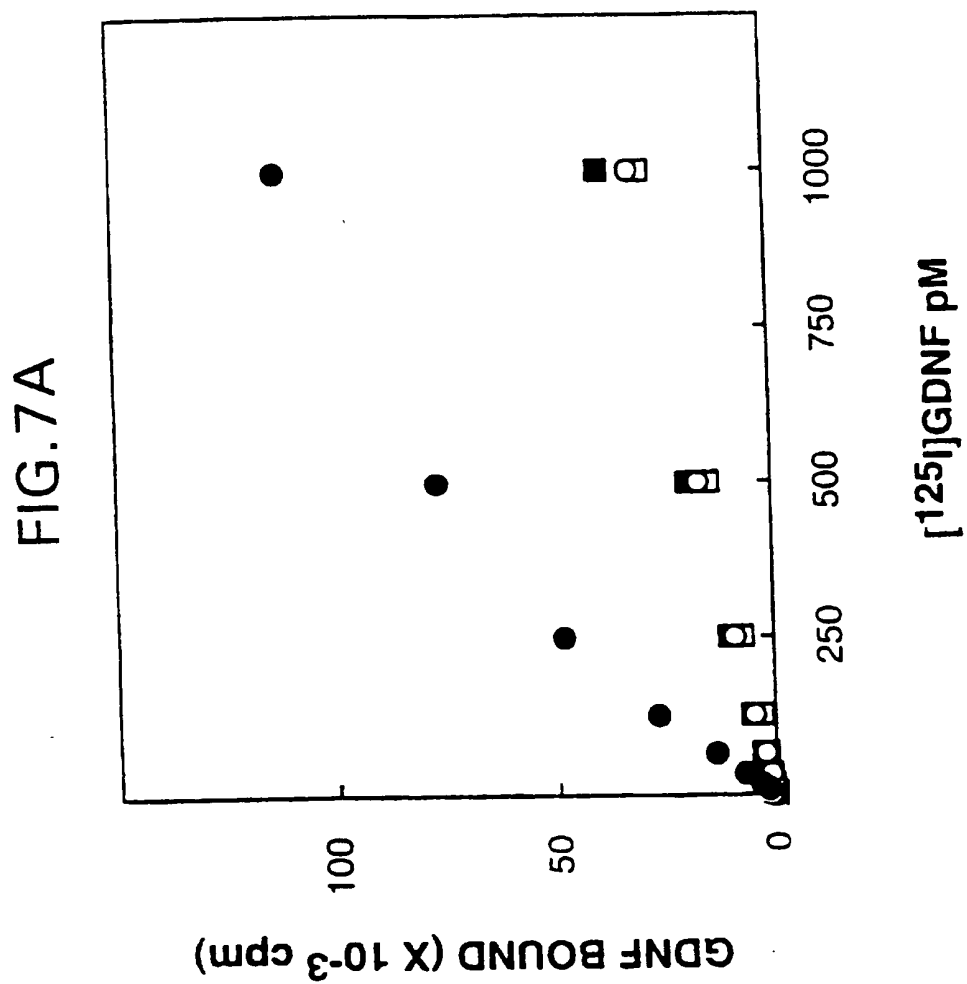
FIG. 5U

	2813		2862
Gdnfr	GTGCAAGCGT GCATACCTGT GGAGGGAAC TGGGGCTGCT TGTAAATGTT		
29brc	GTGCAAGCGT GCATACCTGT GGAGGGAAC TGGGGCTGCT TGTAAATGTT		
	2863		2912
Gdnfr	CTGCAGCATC TCTTGACACA CTTGTTCATGA CACAATCCAG TACCTTGTT		
29brc	CTGCAGCATC TCTTGACACA CTTGTTCATGA CACAATCCAG TACCTTGTT		
	2913		2962
Gdnfr	TTCAGGTTAT CTGACAAAGG CAGCTTTGAT TGGGACATGG AGGCATGGGC		
29brc	TTCAGGTTAT CTGACAAAGG CAGCTTTGAT TGGGACATGG AGGCATGGGC		
	2963		
Gdnfr	AGGCCGGAA		
29brc	AGGCCGGAA		

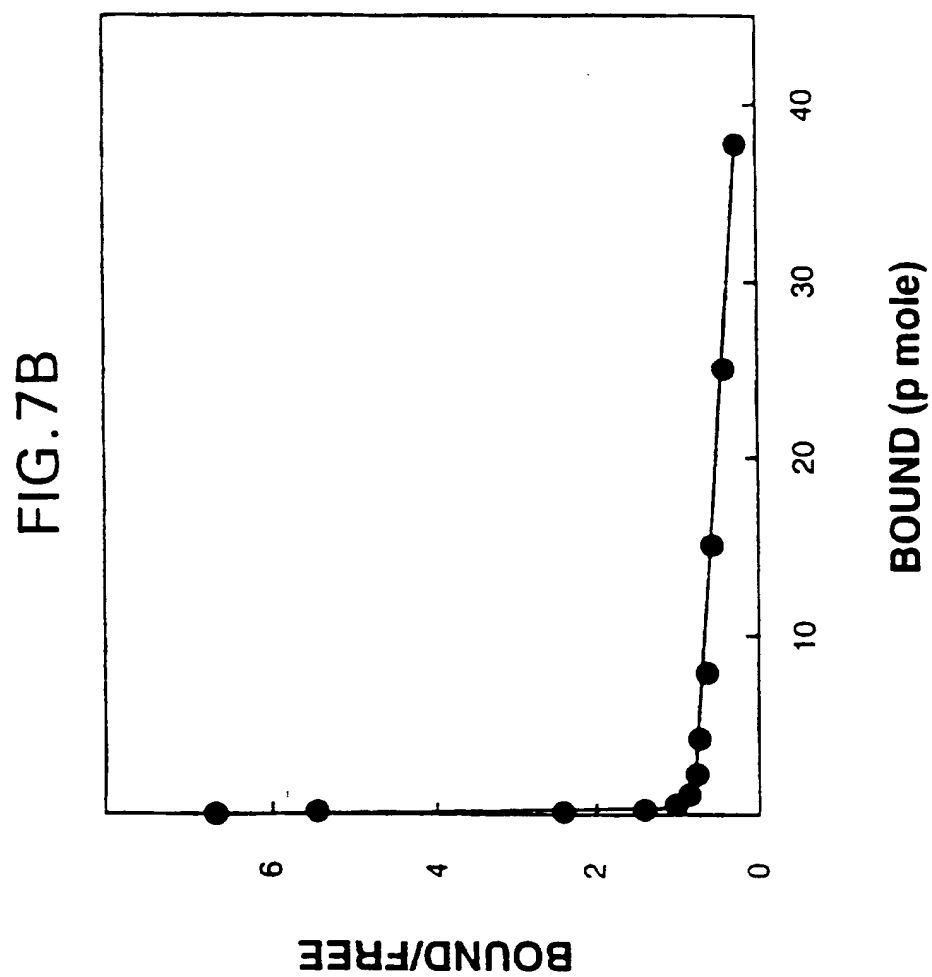
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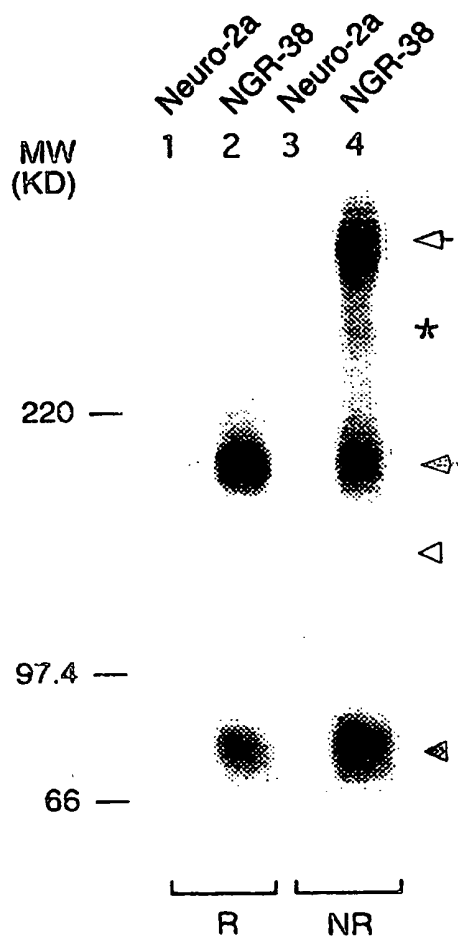


FIG.8

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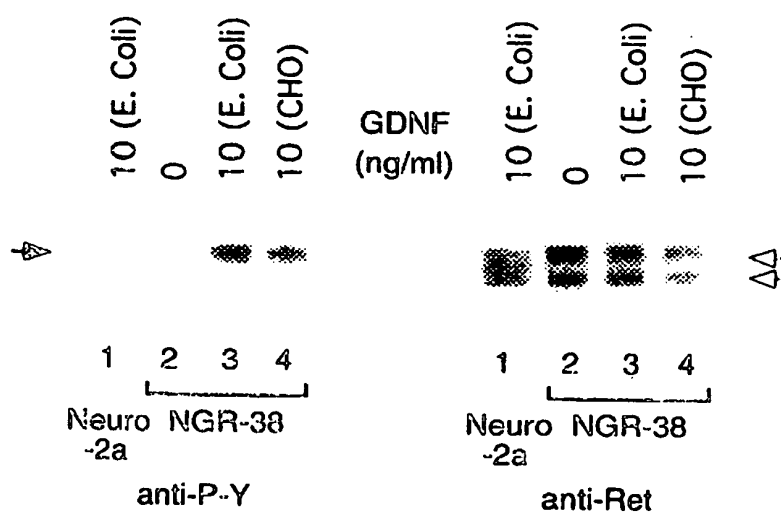


FIG.9A

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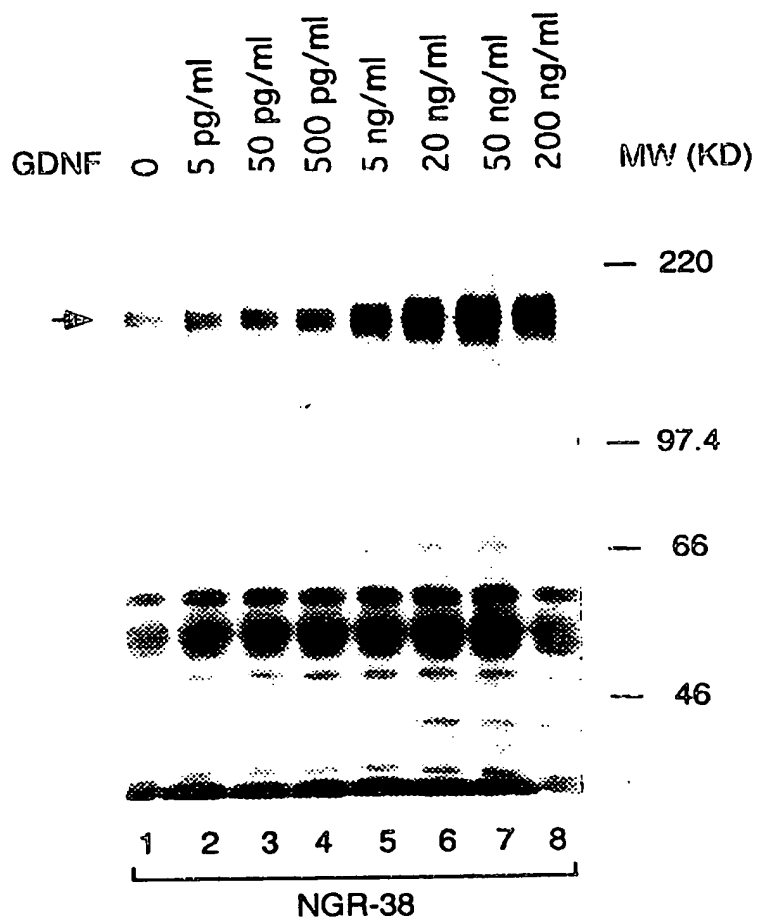


FIG.9B

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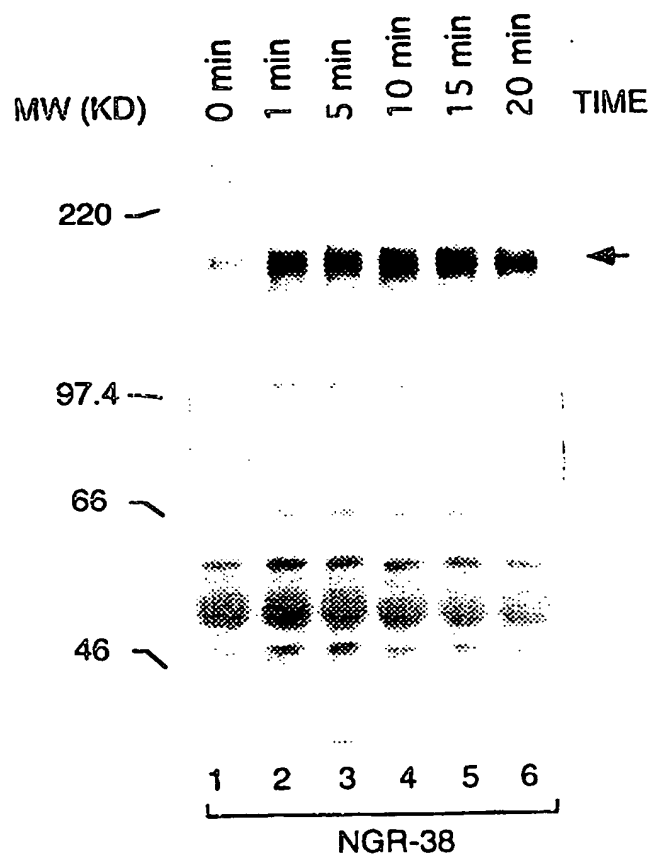


FIG.9C

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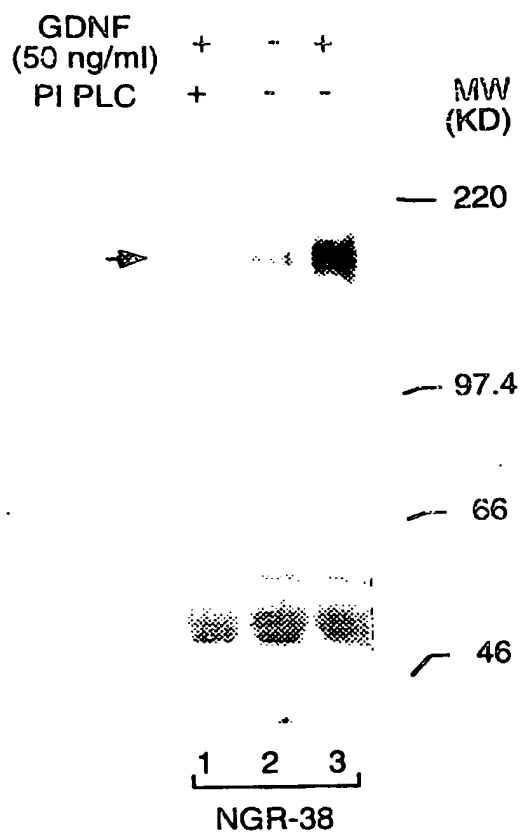


FIG. 10A

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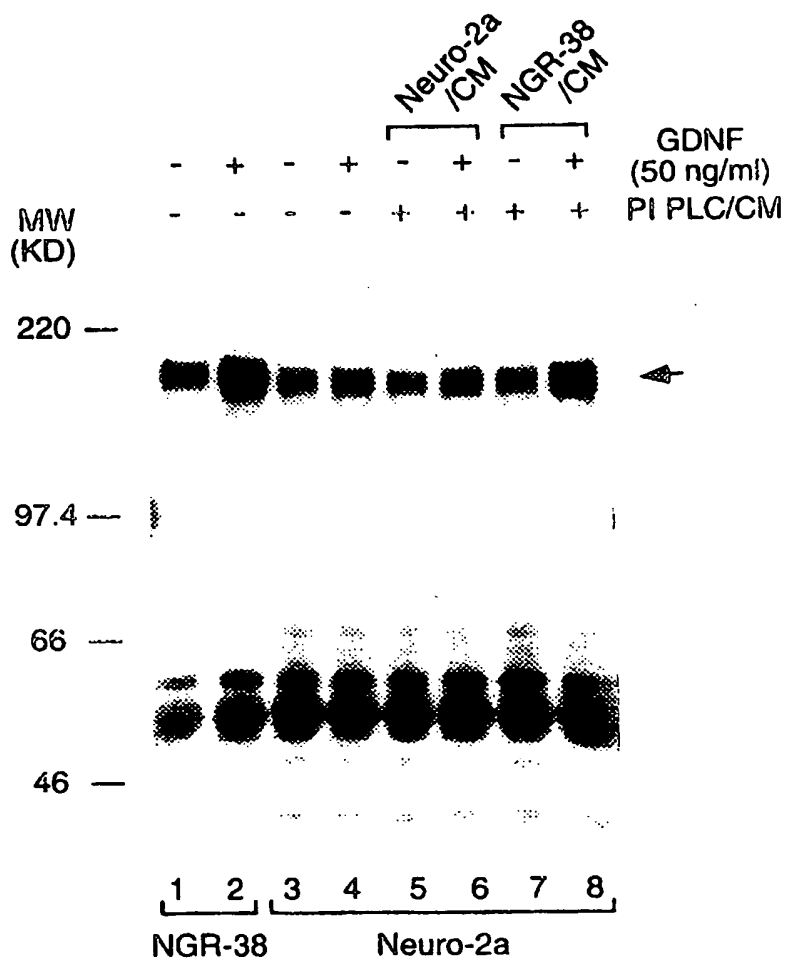


FIG.10B

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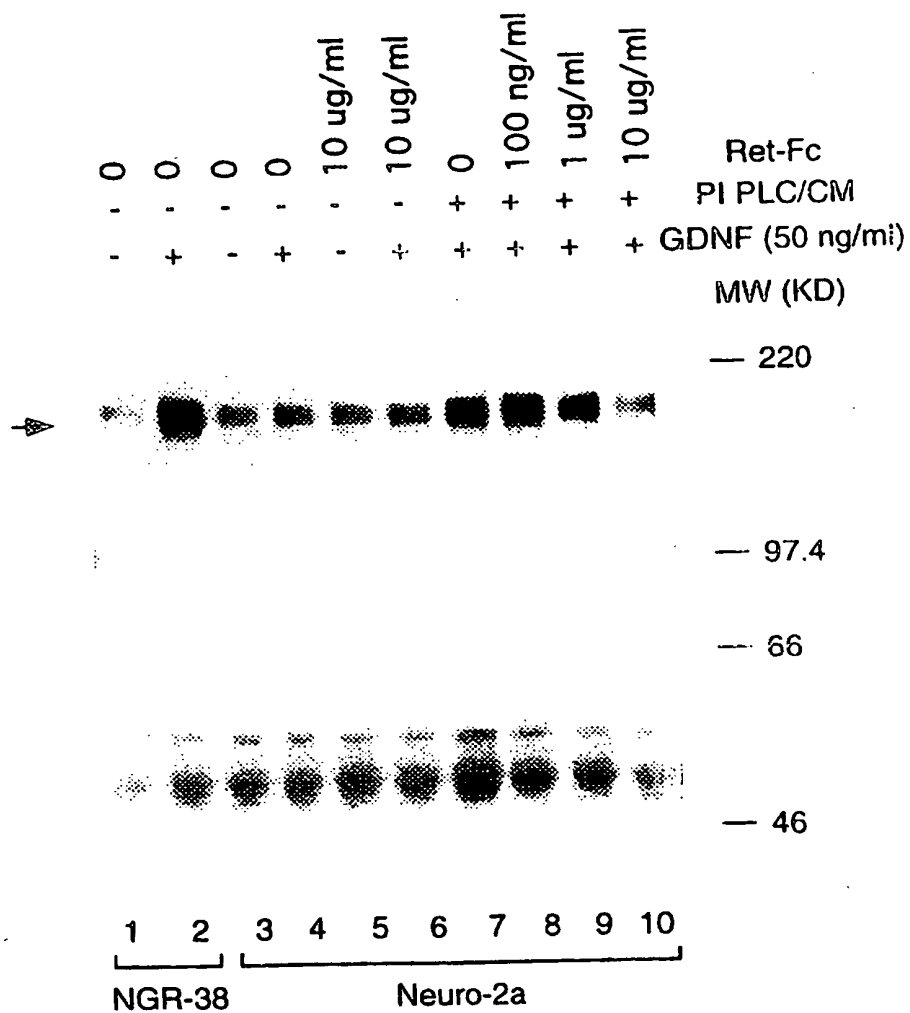


FIG. 11

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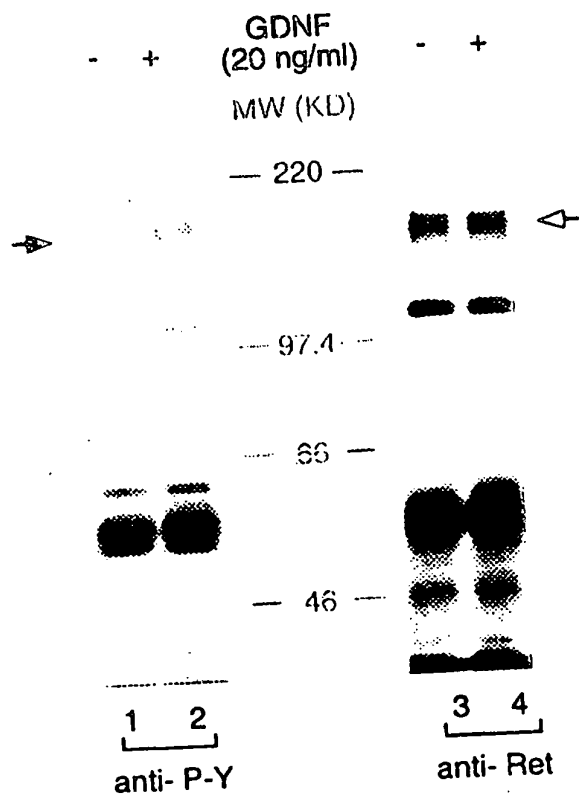
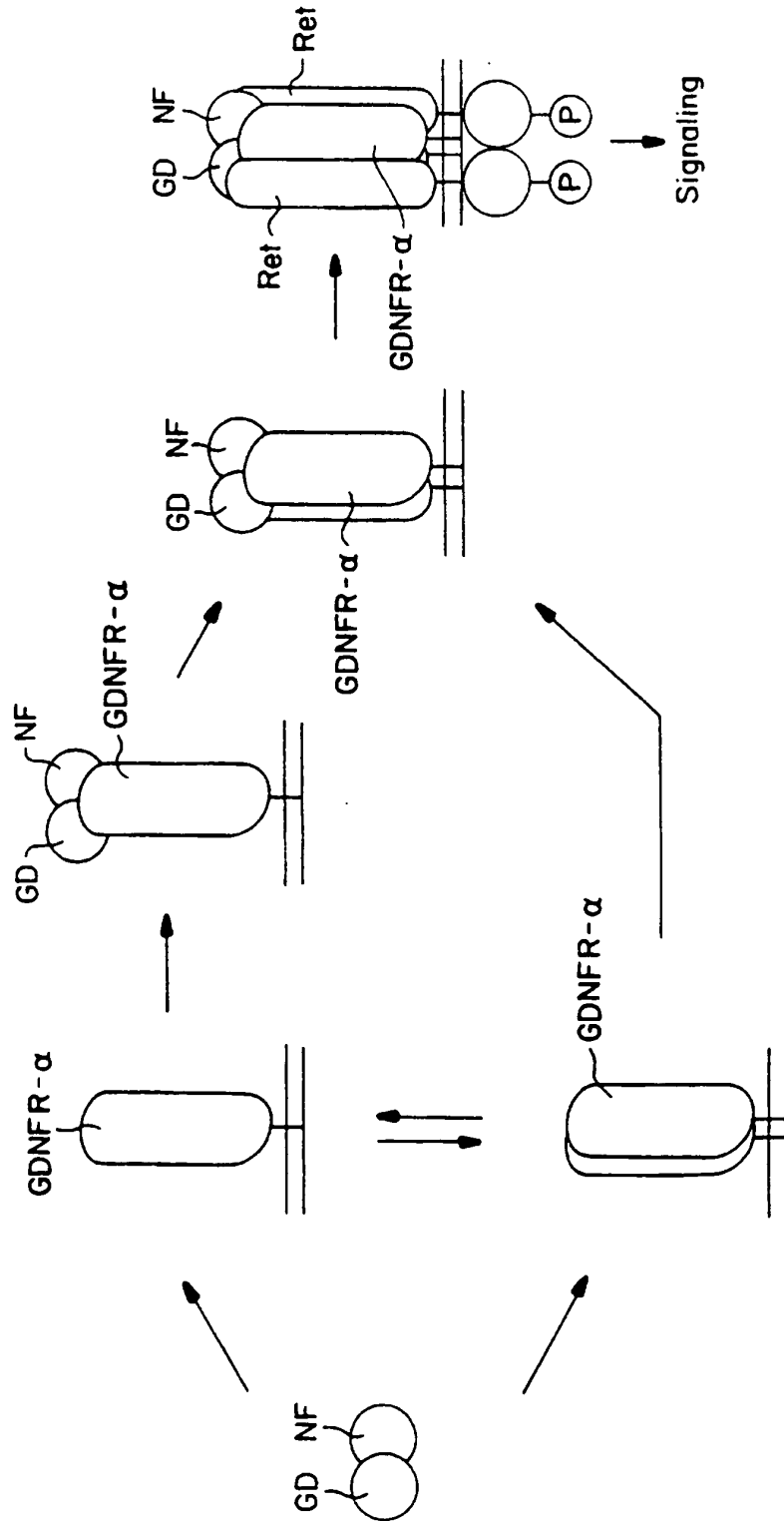


FIG.12

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FIG. 13



INTERNATIONAL SEARCH REPORT

Int. or. Publication No.
PCT/US 97/06281

A. CLASSIFICATION OF SUBJECT MATTER
IPC 6 C12N15/12 C07K14/71 C07K16/28 A61K38/17 C12N1/21
C12N5/10 C12N5/16 G01N33/68 A61K9/48

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)
IPC 6 C07K

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practical, search terms used)

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
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A	WO 93 06116 A (SYNTEX-SYNERGEN NEUROSCIENCE JOINT VENTURE) 1 April 1993 cited in the application see page 91; claims; example 8 ---	46,48
P,X	CELL, vol. 85, 28 June 1996, NA US, pages 1113-1124, XP002036435 SHUQIAN JING ET AL: "GDNF-induced activation of the Ret protein tyrosine kinase is mediated by GDNFR-alpha, a novel receptor for GDNF" see the whole document -----	1-11, 13-35, 49,50

☐ Further documents are listed in the continuation of box C.

☒ Patent family members are listed in annex.

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Date of the actual completion of the international search

5 August 1997

Date of mailing of the international search report

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INTERNATIONAL SEARCH REPORT

International Application No.

PCT/US 97/06281

Box I Observations where certain claims were found unsearchable (Continuation of item 1 of first sheet)

This International Search Report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:

1. ☒ Claims Nos. because they relate to subject matter not required to be searched by this Authority, namely:
Please see Further Information sheet enclosed.
2. ☐ Claims Nos. because they relate to parts of the International Application that do not comply with the prescribed requirements to such an extent that no meaningful International Search can be carried out, specifically:
3. ☐ Claims Nos. because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a).

Box II Observations where unity of invention is lacking (Continuation of item 2 of first sheet)

This International Searching Authority found multiple inventions in this international application, as follows:

1. ☐ As all required additional search fees were timely paid by the applicant, this International Search Report covers all searchable claims.
2. ☐ As all searchable claims could be searched without effort justifying an additional fee, this Authority did not invite payment of any additional fee.
3. ☐ As only some of the required additional search fees were timely paid by the applicant, this International Search Report covers only those claims for which fees were paid, specifically claims Nos.:
4. ☐ No required additional search fees were timely paid by the applicant. Consequently, this International Search Report is restricted to the invention first mentioned in the claims; it is covered by claims Nos.:

Remark on Protest

- ☐ The additional search fees were accompanied by the applicant's protest.
- ☐ No protest accompanied the payment of additional search fees.

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International Application No. PCT/US 97/06281

FURTHER INFORMATION CONTINUED FROM PCT/ISA/210

Remark: Although claims 37-40 are directed a method of treatment of the human/animal body (Rule 39.I IV, PCT) the search has been carried out and based on the alleged effects of the compound/composition.

INTERNATIONAL SEARCH REPORT

Information on patent family members

International Application No

PCT/US 97/06281

Patent document cited in search report	Publication date	Patent family member(s)	Publication date
WO 9306116 A	01-04-93	AU 679167 B	26-06-97
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